

WEST

Help

Logout

Interrupt

[Main Menu](#) [Search Form](#) [Posting Counts](#) [Show S'Numbers](#) [Edit S'Numbers](#) [Preferences](#) [Cases](#)**Search Results -**

Terms	Documents
L2 same (position 116 or position 118 or 116 or 118)	4

Database:

US Patents Full-Text Database	▲
US Pre-Grant Publication Full-Text Database	
JPO Abstracts Database	
EPO Abstracts Database	
Derwent World Patents Index	
IBM Technical Disclosure Bulletins	▼

Search:

L3	▲
	▼

[Refine Search](#)

Recall Text

Clear

Search HistoryDATE: Tuesday, July 01, 2003 [Printable Copy](#) [Create Case](#)**Set Name Query**

side by side

Hit Count Set Name

result set

DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ

<u>L3</u>	L2 same (position 116 or position 118 or 116 or 118)	4	<u>L3</u>
<u>L2</u>	L1 same (mutant or variant)	218	<u>L2</u>
<u>L1</u>	xylanase	2169	<u>L1</u>

END OF SEARCH HISTORY

THIS PAGE BLANK (USPTO)

WEST[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 4 of 4 returned.**☐ 1. Document ID: US 6228983 B1

L3: Entry 1 of 4

File: USPT

May 8, 2001

US-PAT-NO: 6228983

DOCUMENT-IDENTIFIER: US 6228983 B1

**** See image for Certificate of Correction ****

TITLE: Human respiratory syncytial virus peptides with antifusogenic and antiviral activities

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KAMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	------	-----------	-------

☐ 2. Document ID: US 6093794 A

L3: Entry 2 of 4

File: USPT

Jul 25, 2000

US-PAT-NO: 6093794

DOCUMENT-IDENTIFIER: US 6093794 A

TITLE: Isolated peptides derived from the Epstein-Barr virus containing fusion inhibitory domains

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KAMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	------	-----------	-------

☐ 3. Document ID: US 6060065 A

L3: Entry 3 of 4

File: USPT

May 9, 2000

US-PAT-NO: 6060065

DOCUMENT-IDENTIFIER: US 6060065 A

TITLE: Compositions for inhibition of membrane fusion-associated events, including influenza virus transmission

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KAMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	------	-----------	-------

☐ 4. Document ID: US 5871730 A

L3: Entry 4 of 4

File: USPT

Feb 16, 1999

US-PAT-NO: 5871730

DOCUMENT-IDENTIFIER: US 5871730 A

TITLE: Thermostable xylanase DNA, protein and methods of use

THIS PAGE BLANK (USPTO)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	RMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	-----	-----------	-------

[Generate Collection](#)[Print](#)

Terms	Documents
L2 same (position 116 or position 118 or 116 or 118)	4

Display Format:

-

[Change Format](#)[Previous Page](#)[Next Page](#)

THIS PAGE BLANK (USPTO)

=> d his

(FILE 'HOME' ENTERED AT 13:14:21 ON 01 JUL 2003)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI,
BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,
CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB,
DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 13:15:15 ON
01 JUL 2003

SEA XYLANASE

1 FILE ADISCTI
1393 FILE AGRICOLA
29 FILE ANABSTR
63 FILE AQUASCI
758 FILE BIOBUSINESS
58 FILE BIOCOMMERCE
3395 FILE BIOSIS
2264 FILE BIOTECHABS
2264 FILE BIOTECHDS
1429 FILE BIOTECHNO
1715 FILE CABA
18 FILE CANCERLIT
5587 FILE CAPLUS
825 FILE CEABA-VTB
7 FILE CEN
26 FILE CIN
106 FILE CONFSCI
13 FILE CROPB
24 FILE CROPU
3 FILE DDFB
8 FILE DDFU
1949 FILE DGENE
3 FILE DRUGB
8 FILE DRUGU
23 FILE EMBAL
1311 FILE EMBASE
1207 FILE ESBIODASE
49 FILE FEDRIP
5 FILE FOREGE
376 FILE FROSTI
1111 FILE FSTA
1272 FILE GENBANK
3 FILE HEALSAFE
389 FILE IFIPAT
493 FILE JICST-EPLUS
1538 FILE LIFESCI
1236 FILE MEDLINE
2 FILE NIOSHTIC
51 FILE NTIS
1 FILE NUTRACEUT
13 FILE OCEAN
1911 FILE PASCAL
12 FILE PHIN
110 FILE PROMT
4 FILE RDISCLOSURE
2997 FILE SCISEARCH
547 FILE TOXCENTER
1342 FILE USPATFULL
36 FILE USPAT2
404 FILE VETU
655 FILE WPIDS
655 FILE WPINDEX

THIS PAGE BLANK (USPTO)

L1

QUE XYLANASE

FILE 'CAPLUS, BIOSIS, SCISEARCH, BIOTECHDS, DGENE, PASCAL, CABA, LIFESCI,
BIOTECHNO, AGRICOLA, EMBASE, GENBANK, MEDLINE, ESBIODASE, FSTA' ENTERED
AT 13:16:18 ON 01 JUL 2003

L2 2233 S L1 AND (VARIANT OR MUTANT)
L3 2880 S L1 AND (VARIAN? OR MUTA?)
L4 33 S L3 AND (POSITION 116 OR POSITION 118 OR 116 OR 118)
L5 0 S L1 AND (POSITION 11 OR 11D)
L6 4 S L1 AND (POSITION 144R OR POSITION 144 OR POSITION 161R OR 161
L7 21 DUP REM L4 (12 DUPLICATES REMOVED)
L8 21 DUP REM L4 (12 DUPLICATES REMOVED)
L9 4 DUP REM L6 (0 DUPLICATES REMOVED)

THIS PAGE BLANK (USPTO)

=> d 19 ibib ab 1-4

L9 ANSWER 1 OF 4 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI

ACCESSION NUMBER: 2003-01501 BIOTECHDS

TITLE: Bleaching of chemical pulp involves, exposing chemical pulp to acidic bleaching stage to produce partially bleached pulp and treating with thermophilic, alkalophilic **xylanase** in alkaline extraction stage at preset condition; pulp bleaching using recombinant enzyme

AUTHOR: TOLAN J; POPOVICI C; FOODY P J

PATENT ASSIGNEE: IOGEN BIO PROD CORP

PATENT INFO: WO 2002052100 4 Jul 2002

APPLICATION INFO: WO 2001-CA1837 19 Dec 2001

PRIORITY INFO: US 2000-258163 22 Dec 2000; US 2000-258163 22 Dec 2000

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2002-599582 [64]

AB DERWENT ABSTRACT:

NOVELTY - A chemical pulp is bleached by exposing pulp to an acidic bleaching stage to produce a partially bleached pulp and treating with a thermophilic, alkalophilic **xylanase** in an alkaline extraction stage with a final pH of 8-14.

BIOTECHNOLOGY - Preferred Enzyme: The thermophilic, alkalophilic **xylanase** comprises a genetically modified **xylanase**, comprising a family 11 **xylanase** from *Trichoderma*. The **xylanase** is a genetically modified *Trichoderma reesei*, selected from Trx HML 75A, 105H, 125A, 129E, 132R, 135R, 144R, 157D, 161R, 162H, 165H; TrxHML 75A, 105H, 125A, 135R, 144R, 157D, 161R, 162H, 165H; TrxHML 75A, 105H, 125A, 129E; and TrxHML 75A, 105H, 125A, 129E, 135R, 144R, 157D, 161R, 162H, 165H (each sequence having 190 amino acids given in the specification), where HML denotes the mutations 10H, 27M and 29L. The **xylanase** comprises BioBrite **xylanase** or a wild type **xylanase**. Preferred Method: The alkaline extraction is performed at 60-120degreesC at a final pH of 9-11.5 for 30-120 minutes. The alkaline extraction is performed using oxygen and/or hydrogen peroxide. 0.1-10 kg of oxygen and hydrogen peroxide is present per ton of pulp. The partially bleached pulp is treated with a second **xylanase** at pH 8-14. The second **xylanase** is identical to the first **xylanase**. The pulp is treated with the first **xylanase** after alkaline oxygen delignification stage. The enzymatic treatment is performed in condition different from the alkaline extraction stage. Alternately, the chemical pulp is exposed to a chemical bleaching stage to produce a partially bleached pulp. The partially bleached pulp is incubated with an extraction filtrate containing the **xylanase** and subsequently washed with water to produce a papricycle washed **xylanase** treated pulp. The papricycle pulp is treated with the **xylanase** at a final pH of 8-14. Then the extraction filtrate is removed from the extract.

USE - For bleaching pulp using **xylanase**.

ADVANTAGE - The method enables to ensure proper mixing of the enzyme with pulp, to control and monitor process conditions such as pH, temperature, enzyme dosage and incubation time. The method does not necessarily require significant changes to existing pulp bleaching equipment, such as purchasing and implementing costly vessels for performing **xylanase** treatment. By carrying out **xylanase** treatment in an alkaline extraction stage, little or no acid is required to adjust the pH of the pulp prior to **xylanase** addition. The reduction or elimination of acid reduces corrosion of mill equipment and the costs associated with a pulp bleaching process. The addition of **xylanase** after an acidic bleaching stage, or before and after a bleaching stage increases the overall effect of enzyme treatment. The pulp bleaching method also reduce the amount of chemicals required to bleach pulp and also reduce the amount of chlorinated effluent waste

THIS PAGE BLANK (USPTO)

produced by a pulp bleaching process.

EXAMPLE - Unbleached hardwood kraft pulp was incubated at 60 degrees C, at initial pH 9.4 for 60 minutes to simulate the conditions of an enzyme treatment stage. The pulp was washed with water. 15 g of sample of pulp was subjected to chlorine dioxide bleaching stage. Chlorine dioxide was added to the pulp and the system was maintained in a heat-sealable plastic bag. The pulp mixture was cooled to 4 degrees C to minimize evaporation. The kappa factor was recommended to be about 0.17 to avoid formation of furans and dioxins. The pulp was adjusted to a 10% consistency with tap water and the initial pH was adjusted to 9.4 with sodium hydroxide. The pulp was heated to 60degreesC and a genetically modified *Trichoderma reesei* **xylanase** (having Trx HML 75A, 105H, 125A, 129E, 132R, 135R, 144R, 157D, 161R, 162H, 165H at amount of 2.0 units/g of pulp with the enzyme stock at 33 units/ml was added to the pulp. Pulp was treated in a similar manner but with a thermophilic, alkalophilic, **xylanase** in the alkaline extraction stage and exhibited a kappa number of 4.8. (61 pages)

L9 ANSWER 2 OF 4 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI

ACCESSION NUMBER: 2002-09767 BIOTECHDS

TITLE: Modified **xylanase** exhibiting increased
thermostability and alkalophilicity useful for industrial
processing e.g. for pulp manufacturing;
vector-mediated gene transfer and expression in host cell
for recombinant protein production and feedstuff
manufacture

AUTHOR: SUNG W L

PATENT ASSIGNEE: NAT RES COUNCIL CANADA

PATENT INFO: WO 2001092487 6 Dec 2001

APPLICATION INFO: WO: 2000-CA769 31 May 2000

PRIORITY INFO: US 2000-213803 31 May 2000

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2002-171435 [22]

AB DERWENT ABSTRACT:

NOVELTY - A modified **xylanase** (I) exhibiting increased
thermostability and alkalophilicity, comprises at least one substituted
amino acid residue at position 75, 104, 105, 125, 129, 132, 135, 144,
157, 161, 162 or 165, where the position is determined from sequence
alignment of (I) with a 190 residue *Trichoderma reesei* **xylanase**
II amino acid sequence (S1), fully defined in the specification, is new.

DETAILED DESCRIPTION - A modified **xylanase** (I) exhibiting
increased thermostability and alkalophilicity, comprises at least one
substituted amino acid residue at position 75, 104, 105, 125, 129, 132,
135, 144, 157, 161, 162 or 165, where the position is determined from
sequence alignment of (I) with a 190 residue *Trichoderma reesei*
xylanase II amino acid sequence (S1), fully defined in the
specification, is new. (I) is characterized as having a maximum effective
temperature (MET) of 69-78 degrees C, and maximum effective pH (MEP) of
5.8-7.6, where (I) is a family 11 **xylanase** obtained from a
Trichoderma sp..

BIOTECHNOLOGY - Preferred Variant: (I) exhibits improved
thermophilicity and/or alkalophilicity, in comparison to a corresponding
native **xylanase**. The substituted amino acid is at position 75
and is selected from non-polar and a polar amino acid e.g. Ala, Cys, Gly
and Thr. (I) is derived from a family 11 **xylanase** e.g. *T.reesei*
xylanase. (I) further comprises a His at position 10, Met at
position 27 and Leu at position 29 (HML). (I) comprises at least one
substituted polar amino acid residue at position 105, e.g. His, Lys and
Arg. (I) further comprises a second substituted non-polar or polar amino
acid residue at position 75. The polar amino acids at **positions**
161, 162 and 165 are selected from Arg, Lys and His, and the
polar amino acid at position 157 is selected from Asp and Glu. (I)
further comprises at least one substituted non-polar amino acid, Ala, at

THIS PAGE BLANK (USPTO)

position 125, and a second substituted acidic amino acid, Glu, at position 129. (I) further comprises a third substituted non-polar amino acid residue (Ala, Cys, Gly and Thr), at position 75, and a fourth substituted polar amino acid residue (His, Lys, and Arg) at position 105. A fifth substituted non-polar amino acid residue, Pro, is present at position 104. Fifth-eleventh substituted polar amino acid residues at positions 132, 135, 144, 157, 161, 162 and 165 are also provided. The MET is 70-75 degrees C, and The pH of MEP is 6.5-7.4. (I) is further characterized as having a maximum effective pH (MEP) is 5.8-7.6. (I) is preferably selected from TrX-161R-162H-165H; TrX-HML-75A; TrX-HML-105H; TrX-HML-105R; TrX-HML-105K; TrX-HML-75A-105H; TrX-HML-75A-105R; TrX-HML-75C-105R; TrX-HML-75G-105R; TrX-HML-75T-105R; TrX-HML-125A; TrX-HML-125A-129E; TrX-HML-75G-105R-125A-129E (TrX-HML-GRAE); TrX-HML-75A-105H-125A-129E (TrX-HML-AHAE); TrX-HML-75G-105H-125A-129E (TrX-HML-GHAE); TrX-HML-75A-105R-125A-129E (TrX-HML-ARAE); TrX-HML-75G-104P-105R-125A-129E (TrX-HML-GPRAE); TrX-HML-75G-104P-105H-125A-129E (TrX-HML-GPHAE); TrX-HML-AHAE-RR; TrX-HML-AHAE-RRR; TrX-HML-AHAE-RRR-DRHH; TrX-HML-AHA-RR-DRHH; and TrX-HML-AHAE-RR-DRHH.

USE - (I) is useful in industrial process such as pulp manufacturing (claimed). (I) is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed.

ADVANTAGE - (I) has improved performance at conditions of high temperature and pH, and exhibits improved thermophilicity and/or alkalophilicity in comparison to a corresponding native **xylanase**

EXAMPLE - For the construction of TrX(92-190), ten overlapping oligonucleotides XyTv-101, XyTv-102, TrX-103, XyTv-104, XyTv-105, XyTv-106, XyTv-107, TrX-108, XyTv-109, XyTv-110, were designed with codon usage frequency imitating that of *Escherichia coli*. The *SalI* and *BglII* cohesive ends of two terminal oligonucleotides enabled the enzymatic ligation of the ten fragments into the linearized plasmid pXYbc. The ten oligonucleotides encoding the TrX(92-190) region of *Trichoderma xylanase* were phosphorylated in a mixture containing 10X standard kinase buffer (0.4 micro-L), 1 mM ATP (4 micro-L), T4 DNA kinase (5 units), and water (3 micro-L). Phosphorylation reactions were carried out for 1 hour at 37 degrees C. The solutions were then combined and heated to 70 degrees C for 10 minutes. After being cooled slowly to room temperature, the combined solutions were added to a mixture of 4 mM ATP (3.5 micro-L), *EcoRI*-*HindIII* linearized plasmid pUC119 and T4 DNA ligase (3.5 micro-L), and incubated at 12 degrees C for 20 hours. Aliquots of the ligation mixture were used to transform *E. coli* HB101 on YT plates containing ampicillin (100 mg/L). For the preparation of a hybridization probe, one of the oligonucleotides, e.g. XyTv-110 (1 micro-L) was phosphorylated with 32P-ATP (3 micro-L) using T4 DNA kinase (1 micro-L), 10X kinase buffer (1 micro-L), and water (4 micro-L) at 37 degrees C for 1 hour. Transformants were selected randomly for hybridization analysis. Colonies were grown on YT plates with ampicillin overnight, and transferred onto nylon filters. They were then denatured and neutralized. After ultraviolet irradiation at 254 nm for 8 minutes, the filters were washed with 6X saline sodium chloride (SSC)-0.05 % Triton X-100 for 30 minutes. Positively hybridized clones with the intermediate plasmid pBcX-TrX were identified by auto-radiographic analysis. (109 pages)

L9 ANSWER 3 OF 4 DGENE (C) 2003 THOMSON DERWENT

ACCESSION NUMBER: AAE18496 Protein DGENE

TITLE: Modified **xylanase** exhibiting increased thermostability and alkalophilicity useful for industrial processing e.g. for pulp manufacturing -

INVENTOR: Sung W L

PATENT ASSIGNEE: (CAN) NAT RES COUNCIL CANADA.

PATENT INFO: WO 2001092487 A2 20011206

109p

APPLICATION INFO: WO 2001-CA769 20010531

PRIORITY INFO: US 2000-213803P 20000531

THIS PAGE BLANK (USPTO)

DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2002-171435 [22]
DESCRIPTION: Trichoderma reesei **xylanase** mutant, TrX-157D-161R-162H-165H.

AB The present invention relates to a modified **xylanase** exhibiting increased thermostability and alkalophilicity. Modified **xylanase** is useful in industrial process such as pulp manufacturing. Modified **xylanase** is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified **xylanase** has improved performance at conditions of high temperature and pH and exhibits improved thermophilicity and/or alkalophilicity in comparison to corresponding native **xylanase**. The present sequence is Trichoderma reesei **xylanase** (TrX) mutant. Note: The present sequence is not shown in the specification but is derived from wild type **xylanase** referred as SEQ ID NO: 16 (AAE18452) and shown in page 80-81 of the specification.

L9 ANSWER 4 OF 4 DGENE (C) 2003 THOMSON DERWENT

ACCESSION NUMBER: AAE18495 Protein DGENE
TITLE: Modified **xylanase** exhibiting increased thermostability and alkalophilicity useful for industrial processing e.g. for pulp manufacturing -
INVENTOR: Sung W L
PATENT ASSIGNEE: (CANA)NAT RES COUNCIL CANADA.
PATENT INFO: WO 2001092487 A2 20011206 109p
APPLICATION INFO: WO 2001-CA769 20010531
PRIORITY INFO: US 2000-213803P 20000531
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2002-171435 [22]
DESCRIPTION: Trichoderma reesei **xylanase** mutant, TrX-161R-162H-165H.

AB The present invention relates to a modified **xylanase** exhibiting increased thermostability and alkalophilicity. Modified **xylanase** is useful in industrial process such as pulp manufacturing. Modified **xylanase** is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified **xylanase** has improved performance at conditions of high temperature and pH and exhibits improved thermophilicity and/or alkalophilicity in comparison to corresponding native **xylanase**. The present sequence is Trichoderma reesei **xylanase** (TrX) mutant. Note: The present sequence is not shown in the specification but is derived from wild type **xylanase** referred as SEQ ID NO: 16 (AAE18452) and shown in page 80-81 of the specification.

THIS PAGE BLANK (US)

=> d his

(FILE 'HOME' ENTERED AT 13:28:19 ON 01 JUL 2003)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 13:28:29 ON 01 JUL 2003

SEA XYLANASE

1 FILE ADISCTI
1393 FILE AGRICOLA
29 FILE ANABSTR
63 FILE AQUASCI
758 FILE BIOBUSINESS
58 FILE BIOCOMMERCE
3395 FILE BIOSIS
2264 FILE BIOTECHABS
2264 FILE BIOTECHDS
1429 FILE BIOTECHNO
1715 FILE CABA
18 FILE CANCERLIT
5587 FILE CAPLUS
825 FILE CEABA-VTB
7 FILE CEN
26 FILE CIN
106 FILE CONFSCI
13 FILE CROPB
24 FILE CROPU
3 FILE DDFB
8 FILE DDFU
1949 FILE DGENE
3 FILE DRUGB
8 FILE DRUGU
23 FILE EMBAL
1311 FILE EMBASE
1207 FILE ESBIODASE
49 FILE FEDRIP
5 FILE FOREGE
376 FILE FROSTI
1111 FILE FSTA
1272 FILE GENBANK
3 FILE HEALSAFE
389 FILE IFIPAT
493 FILE JICST-EPLUS
1538 FILE LIFESCI
1236 FILE MEDLINE
2 FILE NIOSHTIC
51 FILE NTIS
1 FILE NUTRACEUT
13 FILE OCEAN
1911 FILE PASCAL
12 FILE PHIN
110 FILE PROMT
4 FILE RDISCLOSURE
2997 FILE SCISEARCH
547 FILE TOXCENTER
1342 FILE USPATFULL
36 FILE USPAT2
404 FILE VETU
655 FILE WPIDS
655 FILE WPINDEX

QUE XYLANASE

THIS PAGE BLANK (USPTO)

FILE 'CAPLUS, BIOSIS, SCISEARCH, BIOTECHDS, PASCAL, CABA, LIFESCI,
BIOTECHNO, AGRICOLA, EMBASE, MEDLINE, ESBIODASE, FSTA' ENTERED AT
13:30:17 ON 01 JUL 2003

L2 2253 S L1 AND (VARIANT OR MUTA?)
L3 18 S L2 AND (POSITION 116 OR POSITION 118 OR 116 OR 118)
L4 6 DUP REM L3 (12 DUPLICATES REMOVED)

=> log Y

COST IN U.S. DOLLARS

SINCE FILE TOTAL

THIS PAGE BLANK (USPTO)

=> d 14 ibib ab 1-6

L4 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2003:434726 CAPLUS
TITLE: Trichoderma reesei **xylanase** II enzymes with
enhanced thermophilicity and alkalophilicity
INVENTOR(S): Sung, Wing L.
PATENT ASSIGNEE(S): National Research Council of Canada, Can.
SOURCE: PCT Int. Appl., 105 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003046169	A2	20030605	WO 2002-CA1758	20021120
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: US 2001-990874 A 20011121

AB The present invention provides a **xylanase**, or a modified **xylanase** enzyme comprising at least one substituted amino acid residue at a position selected from the group consisting of amino acid 11, 116, 118, 144 and 161, the position detd. from sequence alignment of the modified **xylanase** with Trichoderma reesei **xylanase** II amino acid sequence. The **xylanases** described herein exhibit improved thermophilicity, alkalophilicity, expression efficiency, or a combination thereof, in comparison to a corresponding native **xylanase**. The max. effect temp. is 69-84.degree. and the max effective pH is 5.8-8.4. The improved properties of **xylanase** II muteins are of use in industrial processes, such as paper pulp manuf.

L4 ANSWER 2 OF 6 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI

ACCESSION NUMBER: 2003-01486 BIOTECHDS
TITLE: Novel **xylanase** activity protein, useful in
bleaching process of pulp and in food and animal feed
industry, has enhanced thermostability and alkalophilicity;
recombinant enzyme production via plasmid expression
useful for animal feedstuff
AUTHOR: BENTZIEN J; DAHIYAT B
PATENT ASSIGNEE: XENCOR INC
PATENT INFO: WO 2002038746 16 May 2002
APPLICATION INFO: WO 2001-US48018 9 Nov 2001
PRIORITY INFO: US 2000-710050 10 Nov 2000; US 2000-710050 10 Nov 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2002-608200 [65]

AB DERWENT ABSTRACT:

NOVELTY - A non-naturally occurring **xylanase** activity (XA) protein (I) comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans **xylanase**, where the protein has been modified to exhibit enhanced thermophilicity, alkalophilicity, or thermostability relative to naturally occurring

THIS PAGE BLANK (USPTO)

B.circulans **xylanase**, and has at least 5 amino acid substitutions, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for: (1) a recombinant nucleic acid (II) encoding (I); (2) an expression vector (III) comprising (II); (3) a host cell (IV) comprising (II) or (III); (4) producing (I); (5) a non-naturally occurring XA conformer (V) having a three dimensional backbone structure that substantially corresponds to the three dimensional backbone structure of B.circulans **xylanase**, where the amino acid sequence of the conformer and the amino acid sequence of the B.circulans **xylanase** are less than about 97% identical; (6) a bleaching agent (VI) comprising (I) as an active ingredient; (7) a non-naturally occurring XA amino acid sequence selected from a group as given in the specification; (8) a non-naturally occurring XA nucleic acid sequence selected from a group as given in the specification; and (9) a XA library comprising **variants** of XA, where the **variants** have been altered to exhibit enhanced alkalophilicity, thermophilicity, or thermostability relative to a naturally occurring B.circulans **xylanase**.

WIDER DISCLOSURE - **Variants** of (I) are also disclosed.

BIOTECHNOLOGY - Preparation: (I) is prepared by culturing (IV) under conditions suitable for the expression of (II) and recovering the expressed XA protein. Preferred Protein: (I) comprises at least three amino acid substitutions at positions chosen from 5, 7, 11, 26, 28, 30, 37, 39, 53, 58, 63, 64, 65, 67, 79, 80, 83, 84, 85, 88, 96, 98, 100, 102, 103, 105, 109, 110, 115, 118, 125, 128, 129, 130, 132, 136, 142, 144, 147, 148, 149, 150, 152, 156, 158, 160, 167, 168, 171, 176, 180, and 182. In (V), at least 90% or 100% of the non-identical amino acids are in the core region of the conformer.

USE - A bleaching agent comprising (I) is useful for bleaching pulp, by contacting pulp with the bleaching agent, which further comprises chemical bleaching and/or an alkali extraction before, after or during contacting pulp with the bleaching agent (claimed). XA proteins and nucleic acids are useful in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g., improving the quality of dough, help bread rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors.

ADVANTAGE - (I) is more alkalophilic, thermophilic and thermostable and hydrolyzes a substrate more efficiently than B.circulans **xylanase**.

EXAMPLE - Sequences for novel thermostable, thermophilic and/or alkaliphilic **xylanase** activity (XA) proteins were designed by optimizing residues in the core of the protein, residues around D83, residues around the helix region, and residues around the active site region using Protein Design Automation (PDA) as described in W098/47089. By visual inspection, the following residues were identified as belonging to the Core of Bacillus circulans **xylanase**: Y26, V28, W30, F36, V38, I51, Y53, A55, W58, G62, G64, L66, L68, G70, T72, I77, Y79, V81, Y105, I107, S130, A142, I144, F146, W153, M169, T171, G173, S176, G178, S180, V182, and V184. A rotamer group was assigned to each CORE position which allowed this position to become any phobic residue with the exception of methionine (i.e, Ala, Val, Leu, Ile, Phe, Tyr, and Trp) plus the original wild type residue. In the following PDA design only the CORE residues were allowed to **mutate** to any amino acid rotamer restricted by the definition of the rotamer group assigned to this position. The rest of the protein was treated as a template, with fixed coordinates. An energy cutoff of 50 kcal/mol for the rotamer/template energy was used to exclude unfavorable rotamers. The Van der Waals radius was scaled by a factor of 0.9 and the solvation model 2 as defined by Street and Mayo was used. The ground state rotamer sequence was extracted from all the possible rotamer sequences using the Dead End Elimination (DEE) method. To check for other low energy sequences a Monte Carlo (MC)

THIS PAGE BLANK (USPTO)

search was performed starting from the DEE ground state. The PDA calculation resulted in a ground state sequence given in the specification. This sequence showed 13 **mutations** when compared to the wild type B.circulans **xylanase** sequence, Y26F, V28I, W30F, Y53F, W58F, G64V, Y79F, Y105F, A142L, T171L, S176A, S180A, and V182I. This state showed 93% identity with the complete wild type B.circulans **xylanase** sequence and had 60% identity in the designed positions with the wild type sequence. Using the Monte Carlo technique a list of low energy sequences was generated. Out of the lowest 1000 sequences generated by Monte Carlo none had more than 20 **mutations** from the wild type sequence and out of the lowest 101 sequences none had more than 18 **mutations**. Any protein sequence showing **mutations** at the above positions generated a more stable and/or active XA protein. (121 pages)

L4 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
 ACCESSION NUMBER: 2000:816350 CAPLUS
 DOCUMENT NUMBER: 135:14921
 TITLE: Molecular characterization of xynX, a gene encoding a multidomain **xylanase** with a thermostabilizing domain from Clostridium thermocellum
 AUTHOR(S): Kim, H.; Jung, K. H.; Pack, M. Y.
 CORPORATE SOURCE: Department of Agricultural Chemistry, Sunchon National University, Sunchon, 540-742, S. Korea
 SOURCE: Applied Microbiology and Biotechnology (2000), 54(4), 521-527
 CODEN: AMBIDG; ISSN: 0175-7598
 PUBLISHER: Springer-Verlag
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB A Clostridium thermocellum gene, xynX, coding for a **xylanase** was cloned and the complete nucleotide sequence was detd. The **xylanase** gene of Clostridium thermocellum consists of an ORF of 3261 nucleotide encoding a **xylanase** (XynX) of 1087 amino acid residues (116 kDa). Sequence anal. of XynX showed a multidomain structure that consisted of four different domains: an N-terminal thermostabilizing domain homologous to sequences found in several thermophilic enzymes, a catalytic domain homologous to family 10 glycosyl hydrolases, a duplicated cellulose-binding domain (CBD) homologous to family IX CBDs, and a triplicated S-layer homologous domain. A deletion **mutant** of xynX having only the catalytic region produced a **mutant** enzyme XynX-C which retained catalytic activity but lost thermostability. In terms of half-life at 70.degree.C, the thermostability of XynX-C was about six times lower than that of the other **mutant** enzyme, XynX-TC, produced by a **mutant** contg. both the thermostabilizing domain and the catalytic domain. The optimum temp. of XynX-C was about 5-10.degree.C lower than that of XynX-TC.

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 6 Elsevier BIOBASE COPYRIGHT 2003 Elsevier Science B.V.
 ACCESSION NUMBER: 1996016919 ESBIOBASE
 TITLE: The conserved noncatalytic 40-residue sequence in cellulases and hemicellulases from anaerobic fungi functions as a protein docking domain
 AUTHOR: Fanutti C.; Ponyi T.; Black G.W.; Hazlewood G.P.; Gilbert H.J.
 CORPORATE SOURCE: H.J. Gilbert, Dept. of Biological/Nutritional Sci., University of Newcastle upon Tyne, Newcastle upon Tyne NE1 7RU, United Kingdom.
 SOURCE: Journal of Biological Chemistry, (1995), 270/49 (29314-29322)
 CODEN: JBCHA3 ISSN: 0021-9258
 DOCUMENT TYPE: Journal; Article

THIS PAGE BLANK (USPTO)

COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Two cDNAs, designated xynA and manA, encoding **xylanase A (XYLA)** and **mannanase A (MANA)**, respectively, were isolated from a cDNA library derived from mRNA extracted from the anaerobic fungus, *Piromyces*. XYLA and MANA displayed properties typical of endo-beta.1,4-**xylanases** and **mannanases**, respectively. Neither enzyme hydrolyzed cellulosic substrates. The nucleotide sequences of xynA and manA revealed open reading frames of 1875 and 1818 base pairs, respectively, coding for proteins of M(r) 68,049 (XYLA) and 68,055 (MANA). The deduced primary structure of MANA revealed a 458-amino acid sequence that exhibited identity with *Bacillus* and *Pseudomonas fluorescens* subsp. *cellulosa* mannanases belonging to glycosyl hydrolase Family 26. A 40-residue reiterated sequence, which was homologous to duplicated noncatalytic domains previously observed in *Neocallimastix patriciarum* **xylanase A** and endoglucanase B, was located at the C terminus of MANA. XYLA contained two regions that exhibited sequence identity with the catalytic domains of glycosyl hydrolase Family 11 **xylanases** and were separated by a duplicated 40-residue sequence that exhibited strong homology to the C terminus of MANA. Analysis of truncated derivatives of MANA confirmed that the N-terminal 458-residue sequence constituted the catalytic domain, while the C-terminal domain was not essential for the retention of catalytic activity. Similar deletion analysis of XYLA showed that the C-terminal catalytic domain homologue exhibited catalytic activity, but the corresponding putative N-terminal catalytic domain did not function as a **xylanase**. Fusion of the reiterated noncatalytic 40-residue sequence conserved in XYLA and MANA to glutathione S-transferase, generated a hybrid protein that did not associate with cellulose, but bound to 97- and 116-kDa polypeptides that are components of the multienzyme cellulase-hemicellulase complexes of *Piromyces* and *Neocallimastix patriciarum*, respectively. The role of this domain in the assembly of the enzyme complex is discussed.

L4 ANSWER 5 OF 6 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V.DUPLICATE

ACCESSION NUMBER: 1995:25116569 BIOTECHNO

TITLE: Evidence for a general role for non-catalytic thermostabilizing domains in **xylanases** from thermophilic bacteria

AUTHOR: Fontes C.M.G.A.; Hazlewood G.P.; Morag E.; Hall J.; Hirst B.H.; Gilbert H.J.

CORPORATE SOURCE: Dept Biological Nutritional Sciences, University of Newcastle upon Tyne, Newcastle upon Tyne NE1 7RU, United Kingdom.

SOURCE: Biochemical Journal, (1995), 307/1 (151-158)
CODEN: BIJOAK ISSN: 0264-6021

DOCUMENT TYPE: Journal; Article

COUNTRY: United Kingdom

LANGUAGE: English

SUMMARY LANGUAGE: English

AB A genomic library of *Clostridium thermocellum* DNA constructed in λ .ZAPII was screened for **xylanase**-expressing clones. Cross-hybridization experiments revealed a new **xylanase** gene isolated from the gene library, which was designated xynY. The encoded enzyme, **xylanase Y (XYLY)**, displayed features characteristic of an endo-beta.1,4-**xylanase**: the enzyme rapidly hydrolysed oat spelt, wheat and rye arabinoxylans and was active against methylumbelliferyl-beta.-D-cellobioside, but did not hydrolyse any cellulosic substrates. The pH and temperature optima of the enzyme were 6.8 and 75.degree.C respectively, and the recombinant XYLY, expressed by *Escherichia coli* had a maximum M(r) of 116 000. The nucleotide sequence of xynY contained an open reading frame of 3228 bp encoding a protein of predicted M(r) 120 105. The encoded enzyme contained a typical

THIS PAGE BLANK (USPTO)

N-terminal 26-residue signal peptide, followed by a 164 amino acid sequence, designated domain A, that was not essential for catalytic activity. Downstream of domain A was a 351-residue **xylanase** Family F catalytic domain, followed by a 180-residue sequence that exhibited 28% sequence identity with a thermostable domain of *Thermoanaerobacterium saccharolyticum* **xylanase** A. The C-terminal portion of XYLY comprised the 23-residue duplicated docking sequence found in all other *C. thermocellum* plant cell wall hydrolases that are constituents of the bacterium's multienzyme complex, termed the cellulosome, followed by a 286-residue domain which exhibited 32% sequence identity with the N-terminal region of *C. thermocellum* **xylanase** Z. The enzyme did not contain linker sequences found in other *C. thermocellum* plant cell wall hydrolases. Analysis of truncated forms of XYLY and hybrid proteins, comprising segments of XYLY fused to the *E. coli* maltose binding domain, confirmed that XYLY contained a central catalytic domain and an adjacent thermostable domain. The C-terminal domain did not bind to cellulose or xylan. Western blot analysis using antiserum raised against XYLY showed that the **xylanase** was located in the cellulosome and did not appear to be extensively glycosylated. The non-catalytic domains of XYLY are discussed in relation to the general stability of thermophilic **xylanases**.

L4 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1990:192771 CAPLUS

DOCUMENT NUMBER: 112:192771

TITLE: Nucleotide sequence and cloning in *Bacillus subtilis* of the *Bacillus stearothermophilus* pleiotropic regulatory gene *degT*

AUTHOR(S): Takagi, Masahiro; Takada, Hiroki; Imanaka, Tadayuki

CORPORATE SOURCE: Fac. Eng., Osaka Univ., Suita, 565, Japan

SOURCE: Journal of Bacteriology (1990), 172(1), 411-18

CODEN: JOBAAY; ISSN: 0021-9193

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The regulatory gene (*degT*) from *B. stearothermophilus* NCA1503 which enhanced prodn. of extracellular alk. protease (*Apr*) was cloned in *B. subtilis* with pTB53 as a vector. When *B. subtilis* MT-2 (*Npr*- [deficiency of neutral protease] *Apr*+) was transformed with the recombinant plasmid, pDT145, the plasmid carrier produced about three times more alk. protease than did the wild-type strain. In contrast, when *B. subtilis* DB104 (*Npr*-*Apr*-) was used as a host, the transformant with pDT145 could not exhibit any protease activity. After construction of the deletion plasmids, DNA sequencing was done. A large open reading frame was found, and nucleotide sequence anal. showed that the *degT* gene was composed of 1,116 bases (372 amino acid residues, mol. wt. of 41,244). A Shine-Dalgarno sequence was found 9 bases upstream from the open reading frame. A *B. subtilis* strain carrying *degT* showed the following pleiotropic phenomena: (i) enhancement of prodn. of extracellular enzymes such as alk. protease and levansucrase; (ii) repression of autolysin activity; (iii) decrease of transformation efficiency for *B. subtilis* (competent cell procedure); (iv) altered control of sporulation; (v) loss of flagella; and (vi) abnormal cell division. When *B. stearothermophilus* SIC1 was transformed with the recombinant plasmid carrying *degT*, the transformants exhibited abnormal cell division. These phenomena are similar to those of the phenotypes of *degSU*(Hy) (hyperprodn.), *degQ*(Hy), and *degR* mutants of *B. subtilis*. However, the amino acid sequence of the *degT* product (*DegT*) is different from those of the reported gene products. Furthermore, *DegT* includes a hydrophobic core region in the N-terminal portion (amino acid nos. 50-160), a consensus sequence for a DNA binding region (amino acid nos. 160-179), and a region homologous to transcription activator proteins (amino acid nos. 351-366). The membrane protein *DegT* may function as a sensor protein and transfer the signal of environmental stimuli to the regulatory region of target genes to activate or repress transcription of the genes.

THIS PAGE BLANK (USPTO,

Hart, Edward

From: Rao, Manjunath N.
Sent: Tuesday, July 01, 2003 11:44 AM
To: Hart, Edward
Subject: Sequence search print out for 09/990,874

Hello Ed,

Below is the request regarding the application I mentioned in our phone conversation. In this case I am looking for variants and therefore I am not interested in 100% matches. Please rerun the search and provide me a print out of those results that have 3-10 or 3-15 mismatches in them. Please provide a print of at least 30-40 such results from each database. Thanks for all your help. If this is confusing to you please call me.

Thanks
Manjunath

From: Manjunath N. Rao
Art Unit 1652, Room 10A11
Mail Box in Room 10D 01
Phone: 306-5681

Date: 5-7-03

Please search the following as soon as possible for application with serial number **09/990874**

SEQ ID NO:16 against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Manjunath N. Rao, Ph.D.
Biotechnology Patent Examiner
Art Unit 1652, Room 10A11
Mail Box in 10D01
Crystal Mall 1, USPTO.

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 11:47:38 ; Search time 27 Seconds

(without alignments)
207.050 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 OTIQPCTGYNMGYFYSTWMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata1/1aa/backfilsl.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1045	100.0	190	1	US-08-044-621D-26	Sequence 26, App1
2	1045	100.0	190	1	US-08-709-912-16	Sequence 16, App1
3	1045	100.0	190	2	US-09-047-370-16	Sequence 16, App1
4	1045	100.0	223	2	US-08-121-436A-2	Sequence 2, App1
5	1035	99.0	190	1	US-08-709-912-17	Sequence 17, App1
6	1035	99.0	190	2	US-09-047-370-17	Sequence 17, App1
7	1032	98.8	190	1	US-08-044-621D-27	Sequence 27, App1
8	1016	97.2	223	4	US-09-254-733-7	Sequence 7, App1
9	996	95.3	190	1	US-08-044-621D-28	Sequence 28, App1
10	996	95.3	190	1	US-08-709-912-14	Sequence 14, App1
11	996	95.3	190	2	US-09-047-370-14	Sequence 14, App1
12	721.9	69.1	261	4	US-08-768-373-2	Sequence 2, App1
13	665.9	63.7	225	1	US-08-290-979A-8	Sequence 8, App1
14	656.9	62.9	230	4	US-08-768-373-4	Sequence 4, App1
15	635.9	60.9	225	4	US-08-886-765-2	Sequence 2, App1
16	635.9	60.9	225	4	US-09-115-660-2	Sequence 2, App1
17	631.6	60.4	231	2	US-08-902-655A-6	Sequence 6, App1
18	631.6	60.4	231	2	US-08-507-431-6	Sequence 6, App1
19	631.6	60.4	236	3	US-09-116-622-6	Sequence 6, App1
20	631.6	60.4	236	4	US-09-219-277-6	Sequence 6, App1
21	620.9	59.4	227	4	US-09-599-661-6	Sequence 6, App1
22	620.9	59.4	227	1	US-08-458-023B-4	Sequence 4, App1
23	608.7	58.2	189	1	US-08-709-912-13	Sequence 13, App1
24	608.7	58.2	189	1	US-09-047-370-13	Sequence 13, App1
25	597.5	57.2	344	2	US-08-468-812-2	Sequence 2, App1
26	597.5	57.2	344	4	US-08-590-563-2	Sequence 2, App1
27	597.4	57.2	206	1	US-08-315-695-19	Sequence 19, App1

28	593.4	56.8	215	1	US-08-044-621D-34	Sequence 34, App1
29	591.4	56.6	191	1	US-08-709-912-10	Sequence 10, App1
30	591.4	56.6	191	2	US-09-047-370-10	Sequence 10, App1
31	568.3	54.4	197	1	US-08-044-621D-29	Sequence 29, App1
32	568.3	54.4	197	1	US-08-709-912-9	Sequence 9, App1
33	568.3	54.4	197	2	US-09-047-370-9	Sequence 9, App1
34	543.9	52.0	278	3	US-09-260-283-2	Sequence 2, App1
35	533.3	51.0	211	1	US-08-575-664-1	Sequence 1, App1
36	533.3	51.0	211	2	US-08-963-500-1	Sequence 1, App1
37	533.2	51.0	216	1	US-08-315-695-20	Sequence 20, App1
38	532.9	51.0	368	3	US-08-591-685-13	Sequence 13, App1
39	532.2	50.9	200	1	US-07-744-570B-2	Sequence 2, App1
40	531.5	50.9	189	1	US-08-044-621D-33	Sequence 33, App1
41	531	50.8	191	1	US-08-044-621D-35	Sequence 35, App1
42	529.5	50.7	189	1	US-08-709-912-12	Sequence 12, App1
43	529.5	50.7	189	2	US-09-047-370-12	Sequence 12, App1
44	529	50.6	191	1	US-08-709-912-11	Sequence 11, App1
45	529	50.6	191	2	US-09-047-370-11	Sequence 11, App1

ALIGNMENTS

RESULT 1
US-08-044-621D-26
; Sequence 26, Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Makarchuk
; APPLICANT: Wing L. Sung
; APPLICANT: Makoto Yaeguchi
; APPLICANT: Robert L. Campbell
; APPLICANT: David R. Rose
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gowling, Strathly & Henderson
; STREET: Suite 2600, 160 Elgin Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1P 1C3
; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,621D
; FILING DATE: April 8, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy A. Erratt
; REGISTRATION NUMBER: 34,076
; REFERENCE/DOCKET NUMBER: 08-863796
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 613-786-0199
; TELEFAX: 613-563-9869
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190
; TYPE: Amino Acid
; STRANDEDNESS: No
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: NO
; HYPOTHEICAL: NO
; ANTI-SENSE: NO

FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Trichoderma reesei, XYN II, 21KD, PI 9.0
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Torronene, A., Mach, R.L., Messner, R.,
AUTHORS: Gonzalez, R., Kalkkinen, N., Harkki, A.,
AUTHORS: Kubicek, C.P.
TITLE:
JOURNAL: Bio/Technology
VOLUME: 10
ISSUE:
PAGES: 1461-1465
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTTQPGTGYNNNGYFYSYWMDHGGVYTTNGPGGQFSYVMSNSGNEFYVGKMGQPTKKKVI 60
1 OTTQPGTGYNNNGYFYSYWMDHGGVYTTNGPGGQFSYVMSNSGNEFYVGKMGQPTKKKVI 60
DB 1 OTTQPGTGYNNNGYFYSYWMDHGGVYTTNGPGGQFSYVMSNSGNEFYVGKMGQPTKKKVI 60
QY 61 NFSGSYVNPNGNSYLSYVGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYVNPNGNSYLSYVGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNOPSITIGTATFYQWYSVRNRHSSGSVNTANHFMAAQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNOPSITIGTATFYQWYSVRNRHSSGSVNTANHFMAAQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 2

US-08-709-912-16
Sequence 16, Application US/08709912
Patent No. 5759840

GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II

PUBLICATION INFORMATION:
AUTHORS: Mach, R. L.
AUTHORS: Messner, R.
AUTHORS: Gonzalez, R.
AUTHORS: Kalkkinen, N.
AUTHORS: Harkki, A.
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-08-709-912-16

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTTQPGTGYNNNGYFYSYWMDHGGVYTTNGPGGQFSYVMSNSGNEFYVGKMGQPTKKKVI 60
1 OTTQPGTGYNNNGYFYSYWMDHGGVYTTNGPGGQFSYVMSNSGNEFYVGKMGQPTKKKVI 60
DB 1 OTTQPGTGYNNNGYFYSYWMDHGGVYTTNGPGGQFSYVMSNSGNEFYVGKMGQPTKKKVI 60
QY 61 NFSGSYVNPNGNSYLSYVGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYVNPNGNSYLSYVGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNOPSITIGTATFYQWYSVRNRHSSGSVNTANHFMAAQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNOPSITIGTATFYQWYSVRNRHSSGSVNTANHFMAAQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3

US-09-047-370-16
Sequence 16, Application US/09047370
Patent No. 5866408

GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194


```

:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/047,370
: FILING DATE:
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/709,912
: FILING DATE: 09-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Olesen Mr. Warren E
: REGISTRATION NUMBER: 27290
: REFERENCE/DOCKET NUMBER: 1039.2000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 758-2400
: TELEFAX: (212) 758-2982
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 190 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
: ORGANISM: Trichoderma reesei
: STRAIN: Xyn II
: PUBLICATION INFORMATION:
: AUTHORS: Tortorene, A
: AUTHORS: Mach, R. L.
: AUTHORS: Messner, R
: AUTHORS: Gonzalez, R
: AUTHORS: Kalkkainen, N
: AUTHORS: Harkki, A
: AUTHORS: Kubicek, C. P.
: JOURNAL: Biotechnology
: VOLUME: 10.
: PAGES: 1461-1465
: DATE: 1992
: US-09-047-370-16

Query Match 100.0%; Score 1045; DB 2: Length 190;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIOPCTGNNNGFYFYMWDGCGVYTTNGPGGQFVNMNSNGNFVGGKGMOPGTNNKYI 60
DB 1 QTIOPCTGNNNGFYFYMWDGCGVYTTNGPGGQFVNMNSNGNFVGGKGMOPGTNNKYI 60
QY 61 NFSGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGEEVTSDSGVYDIYRT 120
DB 61 NFSGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGEEVTSDSGVYDIYRT 120
QY 121 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 180
DB 121 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 4
US-08-121-436A-2
: Sequence 2, Application US/08121436A
: Patent No. 5837515
: GENERAL INFORMATION:
: APPLICANT: Suominen, Pirkko
```

```

:
: APPLICANT: Nevalainen, Helena
: APPLICANT: Saarelainen, Ritva
: APPLICANT: Paloheimo, Marja
: APPLICANT: Lantinen, Tarja
: APPLICANT: Fagerstr m, Richard
: TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Avenue, Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/121,436A
: FILING DATE: 16-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/078,478
: FILING DATE: 18-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FI93/00221
: FILING DATE: 24-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/889,893
: FILING DATE: 29-MAY-1992
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/524,308
: FILING DATE: 16-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Cimbalta, Michele A.
: REGISTRATION NUMBER: 33,851
: REFERENCE/DOCKET NUMBER: 1050.008000C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 223 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-121-436A-2

Query Match 100.0%; Score 1045; DB 2: Length 223;
Best Local Similarity 100.0%; Pred. No. 3.3e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIOPCTGNNNGFYFYMWDGCGVYTTNGPGGQFVNMNSNGNFVGGKGMOPGTNNKYI 60
DB 1 QTIOPCTGNNNGFYFYMWDGCGVYTTNGPGGQFVNMNSNGNFVGGKGMOPGTNNKYI 60
QY 34 QTIOPCTGNNNGFYFYMWDGCGVYTTNGPGGQFVNMNSNGNFVGGKGMOPGTNNKYI 93
DB 34 QTIOPCTGNNNGFYFYMWDGCGVYTTNGPGGQFVNMNSNGNFVGGKGMOPGTNNKYI 93
QY 61 NFSGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGEEVTSDSGVYDIYRT 120
DB 61 NFSGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGEEVTSDSGVYDIYRT 120
QY 94 NFSGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGEEVTSDSGVYDIYRT 153
DB 94 NFSGSYNPNNGNSLYSVYGMRSNPLLEYIIVENFGTYNPSTGATKLGEEVTSDSGVYDIYRT 153
QY 121 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 180
DB 121 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 180
QY 154 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 213
DB 154 QRYNOPSITIGTATFYQYWSVRRNRHSSGSVNTANHNANAAOGLTLGTMDYQIIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190
QY 214 SSGSASITVS 223
DB 214 SSGSASITVS 223

RESULT 5
US-08-709-912-17
```

Sequence 17, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L.
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujle, M
AUTHORS: Watson, D. C.
AUTHORS: Wakarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-08-709-912-17

Query Match 99.0%; Score 1035; DB 1; Length 190;
Best Local Similarity 98.9%; Pred. No. 8.6e-50;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OTTQPGTGVNNGFYFYSYWDGHCAGVYTTNGPGGQFSVNMNSGNTFVGKGMQPGTKNKVI 60
DB 1 OTTQPGTGVNNGFYFYSYWDGHCAGVYTTNGPGGQFSVNMNSGNTFVGKGMQPGTKNKVI 60
QY 61 NFGSGYNPNNGNSLVSYGWRNPLIEYIYENFGTYNPSGARKLGEVTSDDGSVYDIYRT 120
DB 61 NFGSGYNPNNGNSLVSYGWRNPLIEYIYENFGTYNPSGARKLGEVTSDDGSVYDIYRT 120
QY 121 QRVNPSIICTATFYQWYSVRNRHSSGSVNTANHFENAMAQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNPSIICTATFYQWYSVRNRHSSGSVNTANHFENAMAQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190

DB 181 SSGSASITVS 190
RESULT 6
US-09-047-370-17
Sequence 17, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L.
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujle, M
AUTHORS: Watson, D. C.
AUTHORS: Wakarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-09-047-370-17

Query Match 99.0%; Score 1035; DB 2; Length 190;
Best Local Similarity 98.9%; Pred. No. 8.6e-50;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OTTQPGTGVNNGFYFYSYWDGHCAGVYTTNGPGGQFSVNMNSGNTFVGKGMQPGTKNKVI 60
DB 1 OTTQPGTGVNNGFYFYSYWDGHCAGVYTTNGPGGQFSVNMNSGNTFVGKGMQPGTKNKVI 60

QY 61 NFSGSYNPNNGNSYLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGVEYSDGSVYDIYRT 120
|||||
DB 61 NFSGSYNPNNGNSYLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGVEYSDGSVYDIYRT 120
QY 121 ORVNOPSIITGATFFYOYMSVSRNRHSSGSVNTANHFNAMAQGLTLGTMDYOIVAVEGYF 180
|||||
DB 121 ORVNOPSIITGATFFYOYMSVSRNRHSSGSVNTANHFNAMAQGLTLGTMDYOIVAVEGYF 180
QY 181 SSGSASITVS 190
|||||
DB 181 SSGSASITVS 190

RESULT 7
US-08-044-621D-27
Sequence 27, Application US/08044621D
Patent No. 5405769

GENERAL INFORMATION:
APPLICANT: Warren W. Makarchuk
APPLICANT: Wang L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowing, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratic
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
STRAIN: Trichoderma viride, 20KD
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Ujile M., Watson
AUTHORS: D.C., & Makarchuk W.

TITLE: Amino Acid Sequence of the Low-Molecular-
TITLE: Weight Xylanase from Trichoderma viride
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 149-154
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-27

Query Match 98.8%; Score 1032; DB 1; Length 190;
Best Local Similarity 98.8%; Pred. No. 1.3e-49;
Matches 187; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OTIOPGTGNNNGYFYSYWNDDGCGVYTTNGPGGQFSVNMNSGNGFVGKGMQPGTKNKYI 60
|||||
DB 1 OTIOPGTGNNNGYFYSYWNDDGCGVYTTNGPGGQFSVNMNSGNGFVGKGMQPGTKNKYI 60
QY 61 NFSGSYNPNNGNSYLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGVEYSDGSVYDIYRT 120
|||||
DB 61 NFSGSYNPNNGNSYLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGVEYSDGSVYDIYRT 120
QY 121 ORVNOPSIITGATFFYOYMSVSRNRHSSGSVNTANHFNAMAQGLTLGTMDYOIVAVEGYF 180
|||||
DB 121 ORVNOPSIITGATFFYOYMSVSRNRHSSGSVNTANHFNAMAQGLTLGTMDYOIVAVEGYF 180
QY 181 SSGSASITVS 190
|||||
DB 181 SSGSASITVS 190

RESULT 8
US-09-254-733-7
Sequence 7, Application US/09254733
Patent No. 6277596

GENERAL INFORMATION:
APPLICANT: MATANABE, MANABU
APPLICANT: MORIYA, TATSUKI
APPLICANT: AOYAGI, KAORU
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE Cbhl GENES ORIGINATING
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 223
TYPE: PRT
ORGANISM: TRICHODERMA VIRIDE MC300-1
US-09-254-733-7

Query Match 97.2%; Score 1016; DB 4; Length 223;
Best Local Similarity 96.8%; Pred. No. 1.3e-48;
Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTIOPGTGNNNGYFYSYWNDDGCGVYTTNGPGGQFSVNMNSGNGFVGKGMQPGTKNKYI 60
|||||
DB 34 OTIOPGTGNNNGYFYSYWNDDGCGVYTTNGPGGQFSVNMNSGNGFVGKGMQPGTKNKYI 93
QY 61 NFSGSYNPNNGNSYLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGVEYSDGSVYDIYRT 120
|||||
DB 94 NFSGSYNPNNGNSYLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGVEYSDGSVYDIYRT 153
QY 121 ORVNOPSIITGATFFYOYMSVSRNRHSSGSVNTANHFNAMAQGLTLGTMDYOIVAVEGYF 180
|||||
DB 154 ORVNOPSIITGATFFYOYMSVSRNRHSSGSVNTANHFNAMAQGLTLGTMDYOIVAVEGYF 213

OY 181 SSGSASTVS 190
Db 214 SSGSASTVS 223

RESULT 9

US-08-044-621D-28
Sequence 28, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Makarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
City: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: NO, 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
STRAIN: Trichoderma harzianum, 20kd
IMMEDIATE SOURCE:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
AUTHORS: F. Tan L.U.L., Senior D.J., & Saddler
AUTHORS: J.N.
TITLE:
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 435-438
DATE: 1992

DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-28

Query Match 95.3%; Score 996; DB 1; Length 190;
Best Local Similarity 94.7%; Pred. No. 1.2e-47;
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 OTTQPGTGNNGYFYSYWANDHGGVYTYNGPGQFVSVMNSGNEFYGKGWPGTKNKVI 60
Db 1 OTTQPGTGNGYNGYYSYWDGAGVYTYNGGSGSFYVMSNSGNEFYGKGWPGTKNKVI 60
OY 61 NFGSYNPNNGNSLYSYGWSRNPLIEYIYENFTYNTPSGATKLEGVTSDGSVYDIYRT 120
Db 61 NFGSYNPNNGNSLYSYGWSRNPLIEYIYENFTYNTPSGATKLEGVTSDGSVYDIYRT 120
OY 121 QRVNPSIICTATFYQWYSVRNRHSSGSVNTANHFNAMAQGLTGTMDYQIVAVEGYE 180
Db 121 QRVNPSIICTATFYQWYSVRNRHSSGSVNTANHFNAMAQGLTGTMDYQIVAVEGYE 180
OY 181 SSGSASTVS 190
Db 181 SSGSASTVS 190

RESULT 10

US-08-709-912-14
Sequence 14, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Ming L.
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
City: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039,2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
SPRAIN: CBS730.95
FEATURE:
NAME/KEY: Protein
LOCATION: 1..230
OTHER INFORMATION: /label= XLNB
US-08-768-373-4

Query Match 62.9%; Score 656.9; DB 4; Length 230;
Best Local Similarity 64.1%; Pred. No. 7.5e-29;
Matches 118; Conservative 23; Mismatches 42; Indels 1; Gaps 1;

QY 6 GTGYNNGFYFYSWNGHGVTYTNPGGOFYSVMNSGNGFVGKMGQPTKKKVIINFGSS 65
DB 45 GTGTNGWYFYSWNTGGGVTYTNNGSGSYVMONCGFVGKMGRTGAA-ATIKYSON 103
QY 66 YNPNGNSYLSYVMSRNPLIEYIVENFTYNPSTGATKLGVTSDGSYDIYRTQRYNO 125
DB 104 YNPSCNSYLAIGWTRNPLVEYIYESYGTYPSSGAQNLGTFQSDGGRYKAKSTRYNA 163
QY 126 PSITATFTFYQWYSRRNHRSSGSYNTANHNMAAOGLTLCTMDYQIVAAEGYFSSGSA 185
DB 164 PSIECTKFTFYQWYSVRTSKRVGTVTVANHNMAKSKGLNLSHDYQIVATGEGYKSSGSA 223
QY 186 SITV 189
DB 224 SITV 227

RESULT 15
US-08-886-765-2
Sequence 2, Application US/08886765
Patent No. 5817500
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knapp, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58175000 No. 5817500disk of No. 5817500th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-886-765-2

Query Match 60.9%; Score 635.9; DB 2; Length 225;
Best Local Similarity 60.2%; Pred. No. 1e-27;
Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 1 QTIQPGTYNNGFYFYSWNGHGVTYTNPGGOFYSVMNSGNGFVGKMGQPTKKKVI 60
DB 32 QTPNSEGMDHGYYSWMSDGAQATYTNLECGTYEISMGDGNLYGKGNPGLNARAI 91
QY 61 NFGSYNPNNGNSYLSYVMSRNPLIEYIVENFTYNPSTGATKLGVTSDGSYDIYRT 120
DB 92 HEGYVQPNNGSYLAIGWTRNPLVEYIYESYGTYPSSGATDGLTVECDGSYIRLKT 151
QY 121 QVNPSTIGTATFYQWYSRRNHRSSGSYNTANHNMAAOGLTL-CTMDYQIVAAEGY 179
DB 132 TVNMAPSIDGTVOTFYQWYSVRNDRKTSSTVOTGCHFDAMARAGLVNNDHYQIVATIKY 211
QY 180 FSSGSASITVS 190
DB 212 FSSGYARITVA 222

RESULT 16
US-09-115-660-2
Sequence 2, Application US/09115660
Patent No. 6245546
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knapp, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62455460 No. 6245546disk of No. 6245546th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,660
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

```

: APPLICATION NUMBER: 08/886,765
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4324,204-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 225 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-115-660-2

Query Match      60.9%; Score 635.9; DB 4; Length 225;
Best Local Similarity 60.2%; Pred. No. 1e-27;
Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 1 OTTPTGYNNGFYFYVNDGHGVTYTNPGQSFVSNNSGNEFYGGKMGQGTAKKYI 60
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 32 OTTPNSEGMDGYTYSWMSDGAQATYTLLEGTYELISWGDGGLVGGKMGMLNARAI 91
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 61 NFSGSYNPNGNSYLSYGNRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVDYDRT 120
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 92 HFEGVYQPNNSYLAAYGWTNRNPLVEYIVENFGTYDPSGARDLGTVECDGSITRLGRT 151
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 121 QRYNPSTIGTATFTFYWVSRNRHSSGSVNTANFNMAAQGLTLGTMDOYIVAVEGY 179
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 152 TRVNAPSIDGTQTFDDQWYSYRQDKRTSGVTGTGCHFDANARAGLANGDHYQIVATGEY 211
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 180 FSSGSASITVS 190
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 212 FSSGVARITVA 222

RESULT 17
: US-08-902-655A-6
: Sequence 6, Application US/08902655A
: Patent No. 5885819
: GENERAL INFORMATION:
: APPLICANT: Kotod, Lene V.
: APPLICANT: Kaupinen, Markus S.
: APPLICANT: Christgau, Stephan P.
: APPLICANT: Heidt-Hansen, Hans P.
: APPLICANT: Dalboge, Henrik
: APPLICANT: Andersen, Lene N.
: APPLICANT: St, Joan Q.
: APPLICANT: Jacobson, Tina
: APPLICANT: Munk, Niels
: APPLICANT: Mullertz, Anette
: TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
: TITLE OF INVENTION: ASPERGILLUS ACULEATUS
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 58858190 No. 5885819disk of No. 5885819th America, Inc.
: STREET: 405 Lexington Avenue, 64th Floor
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/902,655A
: FILING DATE: 30-July-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
```

```

: NAME: Agris, Cheryl T.
: REGISTRATION NUMBER: 34,086
: REFERENCE/DOCKET NUMBER: 3954,214-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 231 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-902-655A-6

Query Match      60.4%; Score 631.6; DB 2; Length 231;
Best Local Similarity 61.5%; Pred. No. 1.9e-27;
Matches 115; Conservative 26; Mismatches 42; Indels 4; Gaps 3;

QY 7 TGYNNGFYSYWMDG-HGGVYTNPGQGOFSVWMSNGNEFYGGKMGQGTAKKYI 65
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 46 TGYNNGFYSPMTDCAAGDVEYSNGAGSISVTWSASNFVGGKMGPSAHD-ITYSGS 104
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 66 YNP-NGNSYLSYGNRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVDYDRTORY 123
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 105 WTSTGNSNSYLSYGVGTGTPLEVEYITLEDYGEVNPSCATGYKGSYSDGSTYNTATRT 164
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 124 NQPSITIGTATFTFYWVSRNRHSSGSVNTANFNMAAQGLTLGTMDOYIVAVEGYFSSG 183
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 165 NPASITGATFTFYQWYSRNRHSSGSVNTANFNMAAKLGMLGTHVOIVATEGYSSG 224
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 184 SASITVS 190
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 225 SASITVA 231

RESULT 18
: US-08-507-431-6
: Sequence 6, Application US/08507431
: Patent No. 5693518
: GENERAL INFORMATION:
: APPLICANT: Kotod, Lene V.
: APPLICANT: Kaupinen, Markus S.
: APPLICANT: Christgau, Stephan P.
: APPLICANT: Heidt-Hansen, Hans P.
: APPLICANT: Dalboge, Henrik
: APPLICANT: Andersen, Lene N.
: APPLICANT: St, Joan Q.
: APPLICANT: Jacobson, Tina
: APPLICANT: Munk, Niels
: APPLICANT: Mullertz, Anette
: TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
: TITLE OF INVENTION: ASPERGILLUS ACULEATUS
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 56935180 No. 5693518disk of No. 5693518th America, Inc.
: STREET: 405 Lexington Avenue, 64th Floor
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/507,431
: FILING DATE: 15-FEB-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/002,800
: FILING DATE: 25-AUG-1996
: ATTORNEY/AGENT INFORMATION:
```



```

? NAME: Harrington, James J.
? REGISTRATION NUMBER: 38,711
? REFERENCE/DOCKET NUMBER: 3954.204-US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-867-0123
? TELEFAX: 212-878-9655
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 296 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-507-431-6

Query Match
Best Local Similarity 60.4%; Score 631.6; DB 1; Length 296;
Matches 115; Conservative 26; Mismatches 42; Indels 4; Gaps 3;

QY 7 TGYNNGFYYSYNDG-HGVTYTNNGPGGPFSSVMSNSGNFVGKGMQPGTKNKVYNFSGS 65
DB 46 TGYNNGFYYSYNDG-HGVTYTNNGPGGPFSSVMSNSGNFVGKGMQPGSAHD-ITYSGS 104
QY 66 YNF--NGNSYLSYSGSRNPLIEYIVENFGTYNPTSGATKLGVTSDGSVDYVTRQRY 123
DB 105 WTSTGNSNSLYSGWTGTGLVEYILEDDGEYINPGSAGTYKGSYSDGSTYNYITATRT 164
QY 124 NQPSIIGTATFYQYWSVRNRHRSQSVNTANHFNAQAQGLTLGTMDOYQIVAVEGYFSSG 183
DB 165 NAPSIOGTATFYQYWSIRQTKRVGTYTANHFNAKALGMNLGTHNYQIVATEGYSSG 224
QY 184 SASITVS 190
DB 225 SASITVA 231

RESULT 19
US-09-116-622-6
? Sequence 6, Application US/09116622
? Patent No. 6080567
? GENERAL INFORMATION:
? APPLICANT: Kotof, Lene V.
? APPLICANT: Kauppinen, Markus S.
? APPLICANT: Christgau, Stephan
? APPLICANT: Heidt-Hansen, Hans P.
? APPLICANT: Dalboge, Henrik
? APPLICANT: Andersen, Lene N.
? APPLICANT: Si, Joan O.
? APPLICANT: Jacobson, Tina
? APPLICANT: Munk, Niels
? TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
? TITLE OF INVENTION: ASPERGILLUS ACULEATUS
? NUMBER OF SEQUENCES: 42
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. 6080567/disk of No. 6080567th America, Inc.
? STREET: 405 Lexington Avenue, 64th Floor
? CITY: New York
? STATE: New York
? COUNTRY: United States of America
? ZIP: 10174-6401
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/116,622
? FILING DATE: 16-July-1998
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Agtis, Cheryl H.
? REGISTRATION NUMBER: 34,086
? REFERENCE/DOCKET NUMBER: 3954.224-US
```

```

? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-867-0123
? TELEFAX: 212-878-9655
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 296 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-116-622-6

Query Match
Best Local Similarity 60.4%; Score 631.6; DB 3; Length 296;
Matches 115; Conservative 26; Mismatches 42; Indels 4; Gaps 3;

QY 7 TGYNNGFYYSYNDG-HGVTYTNNGPGGPFSSVMSNSGNFVGKGMQPGTKNKVYNFSGS 65
DB 46 TGYNNGFYYSYNDG-HGVTYTNNGPGGPFSSVMSNSGNFVGKGMQPGSAHD-ITYSGS 104
QY 66 YNF--NGNSYLSYSGSRNPLIEYIVENFGTYNPTSGATKLGVTSDGSVDYVTRQRY 123
DB 105 WTSTGNSNSLYSGWTGTGLVEYILEDDGEYINPGSAGTYKGSYSDGSTYNYITATRT 164
QY 124 NQPSIIGTATFYQYWSVRNRHRSQSVNTANHFNAQAQGLTLGTMDOYQIVAVEGYFSSG 183
DB 165 NAPSIOGTATFYQYWSIRQTKRVGTYTANHFNAKALGMNLGTHNYQIVATEGYSSG 224
QY 184 SASITVS 190
DB 225 SASITVA 231

RESULT 20
US-09-219-277-6
? Sequence 6, Application US/09219277
? Patent No. 6197564
? GENERAL INFORMATION:
? APPLICANT: Kotof, Lene V.
? APPLICANT: Kauppinen, Markus S.
? APPLICANT: Christgau, Stephan
? APPLICANT: Heidt-Hansen, Hans P.
? APPLICANT: Dalboge, Henrik
? APPLICANT: Andersen, Lene N.
? APPLICANT: Si, Joan O.
? APPLICANT: Jacobson, Tina
? APPLICANT: Munk, Niels
? APPLICANT: Mullertz, Anette
? TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
? TITLE OF INVENTION: ASPERGILLUS ACULEATUS
? NUMBER OF SEQUENCES: 42
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. 6197564/disk of No. 6197564th America, Inc.
? STREET: 405 Lexington Avenue, 64th Floor
? CITY: New York
? STATE: New York
? COUNTRY: United States of America
? ZIP: 10174-6401
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/219,277
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/116,622
? ATTORNEY/AGENT INFORMATION:
? NAME: Agtis, Cheryl H.
? REGISTRATION NUMBER: 34,086
? REFERENCE/DOCKET NUMBER: 3954.224-US
```

```

: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 296 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-09-219-277-6

```

Query Match	60.4%	Score 631.6;	DB 4;	Length 296;
Best Local Similarity	61.5%	Pred. No. 3e-27;		
Matches 115; Conservative	26;	Mismatches 42;	Indels 4;	Gaps 3;

[illegible]

RESULT 21

US-09-599-661-6

Sequence 6 Application US/09599661
Patent No. 6228630

GENERAL INFORMATION:

APPLICANT: Kotof, Lene V.
APPLICANT: Kaupluen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heidt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: St, Joan O.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6228630disk of No. 6228630disk America, Inc
STREET: 405 Lexington Avenue, 64th Floor
City: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/599,661
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/116,622
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arlis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954,224-US

```

: TELECOMMUNICATION INFORMATION
:
: TELEPHONE: 212-867-0123
:
: TELEFAX: 212-878-9655
:
: INFORMATION FOR SEQ ID NO: 6:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 296 amino acids
:
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: OS-09-599-661-6

```

Query Match	60.4%;	Score 631.6;	DB 4;	Length 296;
Best Local Similarity	61.5%;	Pred. NO. 3e-27;		
Matches 115;	Conservative 26;	Mismatches 42;	Indels 4;	Gaps 3

QY 7 TCGNACNCEFSYNNDCG-HGCVYVYTNPCGQGFVSNMNSCSNPFVGGKGNQPGTKNKVYNFSSG 65
Db 46 TGGSNQYVYSFMTDASGQVEYSNAGGASYVJWSSASNPFVGGKGNMPGSAHD-ITVSGS 104
QY 66 YND--NGNSYLSVYCGMRNPLEEYIVENFCGYNPFSGATKLGESVSDSGSYVDIYPRQV 123
Db 105 WTSTGNSNYSVYVCHTGTPLVEYIILEDYCEYENPGSAGTKSGSYVDGSGTYNLTATRT 164
QY 124 NQPSITIGTATFYQYWSVRRNRHSSGSVYTNANHFMAAQQGLTLCMDYQIVAVEGYFSSG 183
Db 165 NAPSIDGTATFYQYWSIRQTKRVGCTVTJTNANHFMAAKLGMILCTHNYQIVATEGYSSG 224
QY 184 SASITVYS 190
Db 225 SASITVA 231

RESULT 22

US-08-458-023B-4

Sequence 4 Application US/08458023B
Patent No. 5667990
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boomnathan, Katuppan C.
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 5667990disk of No. 5667990th America, Inc
STREET: 405 Lexington Avenue
City: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-023B-4


```

?      HYPOTHEITICAL: NO
?      ANTI-SENSE: NO
?      FRAGMENT TYPE: Internal
?      ORIGINAL SOURCE:
?      ORGANISM: Thermomonospora fusca
?      STRAIN: ttx A
?      PUBLICATION INFORMATION:
?      AUTHORS: Irwin, D
?      AUTHORS: Jung, E. D.
?      AUTHORS: Wilson, D. B.
?      JOURNAL: Appl. Environ. Microbiol.
?      VOLUME: 60
?      PAGES: 763-770
?      DATE: 1994
?
?      US-09-047-370-13
?
Query Match.          58.2%; Score 608.7; DB 2:
Best Local Similarity 56.8%; Pred. NO.2.3e-26;
Matches 104; Conservative 37; Mismatches 39; Indels 3; Gaps 2

```

[illegible]

RESULT 25
 US-08-468-812-2
 Sequence 2, Application US/08468812
 Patent No. 5935836
 GENERAL INFORMATION:
 APPLICANT: Vehmaanper, Jari
 APPLICANT: Mätyl, Aija
 APPLICANT: Fagerström, Richard
 APPLICANT: Lantto, Raija
 APPLICANT: Paloheimo, Marja
 APPLICANT: Suominen, Pirkko
 APPLICANT: Lantinen, Tarja
 APPLICANT: Kristo, Paula
 TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
 TITLE OF INVENTION: of use
 NUMBER OF INVENTION: 25
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNÉ, KESSLER, GOLSTEIN & FOX
 STREET: 1100 NEW YORK AVE., N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,812
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/332,412
 FILING DATE: 31-OCT-1994
 CLASSIFICATION: 435

```

? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/282,001
? FILING DATE: 29-JUL-1994
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Bugalsky, Larry B.
? REGISTRATION NUMBER: 35,086
? REFERENCE/DOCKET NUMBER: 1050.0340002
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-2600
? TELEFAX: 202-371-2540
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 344 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-468-812-2

```

	Query Match	57.2%	Score 597.5;	DB 2;	Length 344;
	Best Local Similarity	53.5%;	Pred. No. 3e-25;		
	Matches	106;	Conservative	35;	Mismatches 42; Indels 15; Gaps 4
QY	5	PGT-----	-GYNNGFFYSYWDNDHGCVITYTNGPGQSFVSVMNSNGNFVGGKGMQ	52	
Db	38	PGTAHADTTITTONOGCYDNGCYFYSFWTAPGVTSWTLHSGGSYSTSVRNRTGNFEVAGKGWS	97		
QY	53	PGTKRNVIFSGSYMPDNCNLSYLVGWSRNFLIEIYIVENFGTVNPSTGATKLGEVPSDG	112		
Db	98	TGR - RTVIYVNASFPNSGNGILTYLGLWRNLPELVETIYESNGTRP - TGYRK - GYVTIDG	154		
QY	113	SVDYIPRGVNOPSIIGTAFPFYQYWSVRNRHSSGSVNTANHEMNAAOQGLLTGDYDQ	172		
Db	155	GTYDIETRYNAPSIEGRTFQQEWSVROOKRTSGTTIGNHPEDAMARAGMNLGSHDYQ	214		
QY	173	IYAVEPSSGSASITVS	190		
Db	215	IMATEBGYSQSGSIVSIS	232		

RESULT 26
 US-08-590-563-2
 : Sequence 2, Application US/08590563
 Patent No. 6300114
 GENERAL INFORMATION:
 APPLICANT: M tyli, Arja
 APPLICANT: Vehmaanger, Jari
 APPLICANT: Fagerstr m, Richard
 APPLICANT: Lantto, Raija
 APPLICANT: Paloheimo, Marja
 APPLICANT: Suominen, Pirkko
 APPLICANT: Laitinen, Tarja
 TITLE OF INVENTION: Production and Secretion of Proteins of
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SPERRE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 STREET: 1100 New York Ave., N.W. Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/590,563
 FILING DATE: 26-JAN-1996
 CLASSIFICATION: 535
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/468,812
 FILING DATE: 06-JUN-1995

REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 215
TYPE: Amino Acid
STRANDEDNESS: No, 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHEICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Streptomyces lividans
STRAIN: Streptomyces lividans, xln B
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Shareck, F., Roy, C., Yaguchi, M.,
AUTHORS: Morosoli, R. & Kluepfel, D.
TITLE:
JOURNAL: Gene
VOLUME: 107
ISSUE:
PAGES: 75-82
DATE: 1991
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-34

Query Match 56.8%; Score 593.4; DB 1; Length 215;
Best Local Similarity 57.1%; Pred. No. 2.1e-25;
Matches 108; Conservative 33; Mismatches 42; Indels 6; Gaps 5;

QY 2 TTPGCGYNNNGYFYSTWNDGCGVYTYTNGCGOFSVNMNSGNGFVGKGMOPCTKKNKYN 61
DB 6 TNEGCT--NNGYYSSTWDSQGTVMNMGSGGQYSTSMRTGTFNFAVGKGMANGR-RTYQ 62
QY 62 FSGSYNPNNGSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRTQ 121
DB 63 YSGSFNPSGNAYLATYGMTSNPLVEYIYVDMNGTYRP-TGEYK-GTVTSDGCTYDIYKTT 120
QY 122 RVNOPSIICTATFYQYVSVRRNHRSSGSVNTANHFANMAOQGLTGTMD-YQIVAVEGYF 180
DB 121 RVNKPVEGSTRFEDQYVSVRQSKRTGCTTTGTHFDMARACMPDGNFSYIMINTEGYQ 180
QY 181 SSGSASITV 189
DB 181 SSGTSSINV 189

RESULT 29
US-08-709-912-10
Sequence 10, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Ming L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr. Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Streptomyces lividans
STRAIN: xln B
PUBLICATION INFORMATION:
AUTHORS: Shareck, F
AUTHORS: Roy, C
AUTHORS: Yaguchi, M
AUTHORS: Morosoli, R
AUTHORS: Kluepfel, D
JOURNAL: Gene
VOLUME: 107
PAGES: 75-82
DATE: 1991
US-08-709-912-10

Query Match 56.8%; Score 591.4; DB 1; Length 191;
Best Local Similarity 56.8%; Pred. No. 2.1e-25;
Matches 107; Conservative 34; Mismatches 42; Indels 6; Gaps 5;

QY 2 TTPGCGYNNNGYFYSTWNDGCGVYTYTNGCGOFSVNMNSGNGFVGKGMOPCTKKNKYN 61
DB 6 TNEGCT--NNGYYSSTWDSQGTVMNMGSGGQYSTSMRTGTFNFAVGKGMANGR-RTYQ 62
QY 62 FSGSYNPNNGSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRTQ 121
DB 63 YSGSFNPSGNAYLATYGMTSNPLVEYIYVDMNGTYRP-TGEYK-GTVTSDGCTYDIYKTT 120
QY 122 RVNOPSIICTATFYQYVSVRRNHRSSGSVNTANHFANMAOQGLTGTMD-YQIVAVEGYF 180
DB 121 RVNKPVEGSTRFEDQYVSVRQSKRTGCTTTGTHFDMARACMPDGNFSYIMINTEGYQ 180
QY 181 SSGSASITV 189
DB 181 SSGTSSINV 189

RESULT 30
US-09-047-370-10
Sequence 10, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Ming L
APPLICANT: Yaguchi Dr., Makoto


```

:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
: ORGANISM: Schizosaccharomyces pombe
: STRAIN: xylanase A
: PUBLICATION INFORMATION:
: AUTHORS: Oku, T
: AUTHORS: Taguchi, M
: AUTHORS: Parise, M
: AUTHORS: Jurasek, L
: JOURNAL: Canadian Fed. Biol. Soc. annual meeting
: PAGES: Abstract #676
: DATE: 1988
:
: US-09-047-370-9
:
Query Match
Best Local Similarity 54.4%; Score 568.3; DB 2; Length 197;
Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

QY 7 TCYNNGYFYSYNNDGCGVYTYNGPGQFYSVMNS-NSGNFVGKGMQPTKKNKVINFGSS 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 TCTDCGYYSMTDGDGATYONNGGSGYTLTWSGNMGLVGKGMNPGASRSISYSGT 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 66 YPNNGNSYLVYGMKRNPLIEYIVNPGTYNPGTATLGEVTSIGSYDITRQVRNQ 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 67 YOPNGNSYLVYGMKRNPLIEYIVNPGTYNPGTATLGEVTSIGSYDITRQVRNQ 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 126 PSIIIGATFYQYVSVRNHRS-----SGSVNTANHFNMAAOGTLTGCT-MDYQIVAVEGY 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 127 PSIDGOTFEQPMVSVNPKKAPGGSISGIVDVQCHDANKGLGMNLSGSHNQIVATEGY 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 FSSGSASITVS 190
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 187 OSSGTATITVT 197
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 34
US-09-260-283-2
: Sequence 2, Application US/09260283
: Patent No. 6083734
: GENERAL INFORMATION:
: APPLICANT: CHUANG, Ming-Hon
: APPLICANT: JENG, King-Song
: APPLICANT: WU, Shaw-Yun
: APPLICANT: LIN, Lung-Shen
: APPLICANT: CHANG, Edward
: TITLE OF INVENTION: NOVEL RECOMBINANT XYLANASE, THE PREPARATION AND USE OF
: FILE REFERENCE: Chuang, et al
: CURRENT APPLICATION NUMBER: US/09/260,283
: CURRENT FILING DATE: 1999-03-02
: EARLIER APPLICATION NUMBER: 87103297
: EARLIER FILING DATE: 1998-03-06
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 278
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Amino acid
: OTHER INFORMATION: Sequence encoded by the recombinant xylanase gene
: OTHER INFORMATION: xylid 1
: US-09-260-283-2

Query Match
Best Local Similarity 52.0%; Score 543.9; DB 3; Length 278;
Matches 102; Conservative 39; Mismatches 48; Indels 11; Gaps 6;

QY 1 QTIOP-GTGYNNGYFYSYNNDGCGVYTYNGPGQFYSVMNSNS-GNFVGKGMQPTKKNK 58
```

```

:
: |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4 QTLSSNSTGTNNGFYTFWKDS-GDASMTLSSGGRYQSSMGSTNNWVGKGMNPNNSR 62
:
QY 59 VINFGST--NPNNGNSYLVYGMKRNPLIEYIVNPGTYNPS--TGATLGEVTSIGSYD 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 VISYSGSYGVDSQNSYALYGMTRSPLEIYVIESYSGYNPASCSCGTDGSPQSDAT 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 YDIYRQRYNOPSITIGTAFYQYVSVRNHRS-----SGSVNTANHFNMAAOGTLTGTM 170
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 YVWRQRYNOPSIDGTFTFYQYVSVRNPKKGFNIGTTFANHVNFASKGLNLGN 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 171 YQIVAVEGYFSSGSASITVS 190
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 183 YQVLATFGYQSRGSSDITVS 202
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 35
US-08-575-964-1
: Sequence 1, Application US/08575964
: Patent No. 5736384
: GENERAL INFORMATION:
: APPLICANT: Fukunaga, No. 5736384yuk1
: APPLICANT: Iwasaki, Yui1
: APPLICANT: Kono, Satoko
: APPLICANT: Kita, Yukio
: APPLICANT: Izumi, Yoshio
: TITLE OF INVENTION: THERMOSTABLE XYLANASE
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: MA USA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/575,964
: FILING DATE: 20-DEC-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Haile, Lisa A.
: REGISTRATION NUMBER: 38,347
: REFERENCE/DOCKET NUMBER: 07898/002001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678-5070
: TELEFAX: 619/678-5099
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 211 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Bacillus sp.
: STRAIN: 2113
: FEATURE:
: OTHER INFORMATION: 1-23 S sig peptide.
: OTHER INFORMATION: 24-211 S mat peptide.
: US-08-575-964-1

Query Match
Best Local Similarity 51.0%; Score 533.3; DB 1; Length 211;
Matches 101; Conservative 28; Mismatches 45; Indels 7; Gaps 5;

QY 14 FYSYNDGCGVYTYNGPGQFYSVMNSNSGNFVGKGMQPTKKNKVINF-SGSYNPNNS 72
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 32 YMOYMTDGGGTATNATNGSGNYSVTWMSVGNFVVGKGMGTGSPTRIVYNAGVWAPSNG 91
QY 73 YLSVYGSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVDYIFRORVNOPSLIGTA 132
Db 92 YLTLYGWTNRSLIEYIVVDSMGTYRP-TGYRK-GTVSDGCTDIYITTMRYNAPSIDGTQ 149
QY 133 TFPQYMSVRNRHSSG---SVNTANHNANAAOGLTLG-TMDYOIVAVEGYFSSGSASIT 188
Db 150 TFPQYMSVRQSKRPTGSNVSITFSNHYNAMRNAGMNLGSSWAVOVLAVEGYQSSGSANVT 209
QY 189 V 189
Db 210 V 210

RESULT 36

US-08-963-500-1
Sequence 1, Application US/08963500
Patent No. 5916795
GENERAL INFORMATION:
APPLICANT: Fukunaga, No. 5916795yuyuki
APPLICANT: Iwasaki, Yoji
APPLICANT: Kono, Satoko
APPLICANT: Kita, Yukio
APPLICANT: Izumi, Yoshiya
TITLE OF INVENTION: THERMOSTABLE XYLANASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963.500
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,964
FILING DATE: 20-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07898/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus sp.
STRAIN: 2113
FEATURE:
OTHER INFORMATION: 1-23 S sig peptide.
US-08-963-500-1

Query Match 51.0%; Score 533.3; DB 2; Length 211;
Best Local Similarity 55.8%; Pred. No. 4e-22;
Matches 101; Conservative 26; Mismatches 45; Indels 7; Gaps 5;

QY 14 FYSYNDHGAGVYTTNGPGQFSVMSNSGNFVGKGMQDPTKKNKYNF-SGYSNPNGNS 72
Db 32 YMOYMTDGGGTATNATNGSGNYSVTWMSVGNFVVGKGMGTGSPTRIVYNAGVWAPSNG 91
QY 73 YLSVYGSRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVDYIFRORVNOPSLIGTA 132
Db 92 YLTLYGWTNRSLIEYIVVDSMGTYRP-TGYRK-GTVSDGCTDIYITTMRYNAPSIDGTQ 149
QY 133 TFPQYMSVRNRHSSG---SVNTANHNANAAOGLTLG-TMDYOIVAVEGYFSSGSASIT 188
Db 150 TFPQYMSVRQSKRPTGSNVSITFSNHYNAMRNAGMNLGSSWAVOVLAVEGYQSSGSANVT 209
QY 189 V 189
Db 210 V 210

RESULT 37

US-08-315-695-20
Sequence 20, Application US/08315695
Patent No. 5591619
GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
TITLE OF INVENTION: Aureobasidium pullulans xylanase, Gene
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315.695
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P.
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 55-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-315-695-20

Query Match 51.0%; Score 533.2; DB 1; Length 216;
Best Local Similarity 50.5%; Pred. No. 4.2e-22;
Matches 101; Conservative 31; Mismatches 50; Indels 18; Gaps 6;

QY 5 PGTGY-----NGYFYSYNDHGAGVYTTNGPGQFSVMSNSGNFVGKGMQDPTKKNKYNF-SGYSNPNGNS 53
Db 21 PGTAHAATTITTTNOTGTGDMYYSFMTDGGGSVMTLNGGGSYSTQMTNCGNFVAGKGMW 80
QY 54 GTNKNKYNFSGNSNPNGNSLSVYGSRNPLIEYIVENFGTYNPSTGATKLGVTSDGS 113
Db 81 GDSN--VRYNGYENPVNGYGLYGTSMPLVEYIVDMNGSYRP-TGYRK-GTVSSDGG 136

[illegible]

RESULT 38

```

US-08-591-685-13
: Sequence 13, Application US/08591685
: Patent No. 6083733
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Thermostable xylanases
: NUMBER OF SEQUENCES: 13
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/591,685
: FILING DATE:
: CLASSIFICATION: 435
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 368 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-591-685-13

```

Query Match	51.0%	Score 532.9;	DB 3,	Length 368;
Best Local Similarity	57.1%;	Pred. No. 1.2e-21;		
Matches 108; Conservative	22;	Mismatches 48;	Indels 11;	Gaps 6

[illegible]

RESULT 39
US-07-744

Sequence 2, Application US/07744570B
Patent No. 5202249
GENERAL INFORMATION:
APPLICANT: Kluepfel, D.
APPLICANT: Morosoli, R.
APPLICANT: Shareck, F.
TITLE OF INVENTION: xylanase for Biobleaching
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael J. Bradley
STREET: 1200 South 47th Street
STREET: Box Number 4023
CITY: Richmond
STATE: California
COUNTRY: United States

```

: ZIP: 94804-0023
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb storage
:
: COMPUTER: IBM
:
: OPERATING SYSTEM: MS-DOS
:
: SOFTWARE: Wordperfect 5.1
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/07/744,570B
:
: FILING DATE: 19910813
:
: CLASSIFICATION: 435
:
: INFORMATION FOR SEQ ID NO: 2:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 200 amino acids
:
: TYPE: AMINO ACID
:
: STRANDEDNESS: Single strand
:
: TOPOLOGY: Circular
:
: US-07-744-570B-2

```

Query Match	50.9%	Score 532.2	DB 1	Length 200
Best Local Similarity	50.5%	Pred. No. 4,1e-22		
Matches 101	Conservative 30	Mismatches 51	Indels 18	Gaps 6

[illegible]

RESULT 40

US-08-044-621D-33
Sequence 33, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erralt

REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 189
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Streptomyces sp.
STRAIN: Streptomyces sp. #36a
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Nagashima M., Okumoto Y. & Okanishi M.
TITLE:
JOURNAL: Trends In Actinomycetologia
VOLUME:
ISSUE:
PAGES: 91-96
DATE: 1989
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-33

Query Match 50.9%; Score 531.5; DB 1; Length 189;
Best Local Similarity 52.1%; Pred. No. 4.1e-22;
Matches 99; Conservative 34; Mismatches 52; Indels 5; Caps 5;

QY 2 TIQPGTYNNGYFYSWNDGCGVTYTNCGGQFVSVMWSNCFVGGKGNQPGTKKKNVIN 61
DB 3 TITNETGY-DGMYTSEFTDGGSVSMTLNCGGSYSTRTWTCGNFVAGKGNANGR-RTVR 60
QY 62 FSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSGTATKLGVTSDGSYYDIYRTQ 121
DB 61 YTGMPNPSGNGYCLGWTSPNPLEYIYVDNMGSYRP-TGETR-GTYHSDGCTYDIYKT 118
QY 122 RVNOPSITGATFYQYVSWRRNHRSSGSVNTANHFNAQAQGLTGTMD-YQIYAVEGYF 180
DB 119 RYNAPSEVPAALDQYVSWRSKVTSGTITTGHNHFDAMARAGNMGNFRYYIMATGEGYQ 178
QY 181 SSGSASTVS 190
DB 179 SSGSSTIVS 188

RESULT 41
US-08-044-621D-35
Sequence 35; Application US/08044621D
GENERAL INFORMATION:
PATENT NO. 5405769
APPLICANT: Warren W. Makarchuk
APPLICANT: Ming L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, Strathly & Henderson

STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erralt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 191
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Streptomyces lividans
STRAIN: Streptomyces lividans, Xln C
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Shareck, F., Roy, C., Yaguchi, M.,
AUTHORS: Morosoli, R. & Kluepfel, D.
TITLE:
JOURNAL: Gene
VOLUME: 107
ISSUE:
PAGES: 75-82
DATE: 1991
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-35

Query Match 50.8%; Score 531; DB 1; Length 191;
Best Local Similarity 53.1%; Pred. No. 4.4e-22;
Matches 102; Conservative 30; Mismatches 50; Indels 10; Caps 6;

QY 2 TIQPGTYNNGYFYSWNDGCGVTYTNCGGQFVSVMWSNCFVGGKGNQPGTKKKNVIN 61
DB 6 TNOTGT---DGMYTSEFTDGGSVSMTLNCGGSYSTQWNTNCGNFVAGKGNSTDCN--VR 60
QY 62 FSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSGTATKLGVTSDGSYYDIYRTQ 121
DB 61 YNGYFNPVNGYCLGWTSPNPLEYIYVDNMGSYRP-TGYR-GTVSSDGGCTYDIYQT 118
QY 122 RVNOPSITGATFYQYVSWRRNHRSSGS--VNTANHFNAQAQGLTGTMD-YQIYAVEG 178
DB 119 RYNAPSEVGTFTQYVSWRSKVTSGTITTGHNHFDAMARAGNMGNFRYYIMATGEG 178

Db 3 TITNETGY-DGMYSFMTDGGGVSMTLNGGGSYSTRMTNCGNFVAGKGMANGR-RTYR 60
QY 62 FSGSYNPNCGNSYLSYVGSNRNPLIEYIYENFCTYIPSTGATKLGCVTSDDGSVYDIYRQ 121
Db 61 YGWFNPNSNGYCGCLYGWTSNPLVEYIYDNNGSYRP-TGYR-CTVSHDGGTYDIYQTT 118
QY 122 RVNOPSITGATFYQYVSVRRNRSSGSVNTANFNMAAOGLLTGTMDOYIV-AVEGYE 180
Db 119 RVNAPSEVEAPAFDQYVSVRSQSVTSCTITTGHNFDAMARAGNMGNFRYIMINATEGY 178
QY 181 SSGSASITVS 190
Db 179 SSGSSNITVS 188

RESULT 44
US-08-709-912-11
Sequence 11, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr., Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Streptomyces lividans
STRAIN: xln C
PUBLICATION INFORMATION:
AUTHORS: Shareck, F
AUTHORS: Roy, C
AUTHORS: Yaguchi, M
AUTHORS: Morosoli, R
AUTHORS: Kluepfel, D
JOURNAL: Gene
VOLUME: 107
PAGES: 75-82

DATE: 1991
US-08-709-912-11
Query Match 50.6%; Score 529; DB 1; Length 191;
Best Local Similarity 52.6%; Pred. No. 5,7e-22;
Matches 101; Conservative 31; Mismatches 50; Indels 10; Gaps 6;

QY 2 TIOPGTGYNNGYFYVYNDGHGVYTNPGGQFSYVWMSNGNFVAGKGMOPGTNRKYN 61
Db 6 TNOGT---DGMYSFMTDGGGVSMTLNGGGSYSTQMTNCGNFVAGKGMSTGDCN--VR 60
QY 62 FSGSYNPNCGNSYLSYVGSNRNPLIEYIYENFCTYIPSTGATKLGCVTSDDGSVYDIYRQ 121
Db 61 YGWFNPNSNGYCGCLYGWTSNPLVEYIYDNNGSYRP-TGYR-CTVSHDGGTYDIYQTT 118
QY 122 RVNOPSITGATFYQYVSVRRNRSSGS--VNTANFNMAAOGLLTGTMDOYIV-AVEG 178
Db 119 RVNAPSEVEGTFTQOQYVSVRSQSVTSCTITTGHNFDAMARAGNMGNFRYIMINATEG 178
QY 179 YFSSGSASITVS 190
Db 179 YOSSSSNITVS 190

RESULT 45
US-09-047-370-11
Sequence 11, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr., Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:

US-08-044-621D-37

Result 48

Sequence 37 Application US/08044621D

Patent No. 5405769

GENERAL INFORMATION:

APPLICANT: Warren W. Makarchuk

APPLICANT: Wing L. Sung

APPLICANT: Makoto Yaguchi

APPLICANT: Robert L. Campbell

APPLICANT: David R. Rose

TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS

TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gowing, Strathly & Henderson

STREET: Suite 2600, 160 Elgin Street

CITY: Ottawa

STATE: Ontario

COUNTRY: Canada

ZIP: K1P 1C3

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 in., 360KB storage

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/044,621D

FILING DATE: April 8, 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Judy A. Erratt

REGISTRATION NUMBER: 34,076

REFERENCE/DOCKET NUMBER: 08-863796

TELECOMMUNICATION INFORMATION:

TELEPHONE: 613-786-0199

TELEFAX: 613-563-9869

TELEX:

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 185

TYPE: Amino Acid

STRANDEDNESS: NO, 5405769 Relevant

TOPOLOGY: Linear

MOLECULE TYPE:

DESCRIPTION: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: NO

ORGANISM: Bacillus subtilis

IMMEDIATE SOURCE:

POSITION IN GENOME:

FEATURE:

PUBLICATION INFORMATION:

AUTHORS: Palce, M.G., Bourbonnais R., Desrochers

AUTHORS: M., Jurasek L., & Yaguchi M.

TITLE:

JOURNAL: Arch. Microbiol.

VOLUME: 144

ISSUE:

PAGES: 201-206

DATE: 1986

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-044-621D-37

Query Match 48.4%; Score 506.2; DB 1; Length 185

Best Local Similarity 53.8%; Ptd. No. 9,6e-21;

```

Matches 98: Conservative 29: Mismatches 47: Indels 8: Gaps 6:
QY 14 FYSTWNDHGCVTTTNGFGGQFVSVMWSNSGNFVGCKGMOPTKKNKLVNF-SCSTNPNGNS 72
   :: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 YQWMTTDDGGCIVANVANGSGCNYSVMWSNTGAFNVYCKGWTGSPFTIYNAGVAPNNG 64
QY 73 YLSAYGWSRNLIEEYIYENFGTYNPSGATKLEVTNSDGSVYDIYRQVRNOPSITG-T 131
   ||::|||::|:|||||::|::|::| | | | | | | | | | | | | | | | | | | |
Db 65 YLTLLGWTWRSPLEIYEVVDSMGTYRP-TGYTK-GTVMSDGGGTYYDLYTTRNAPSIDGDR 122
QY 132 ATFYQWSVRNRHHSSGS--VNTANHPNMAAOGLTGT-MDYQIYAVEGFSSGSASI 187
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 123 TTFQYWSVRQSKRPTGSMATITTSNHNAMKSHGMSWMAIQVMAETEGYSSGSNV 182
QY 188 TV 189
   ||
Db 183 TV 184

RESULT 49
US-08-709-912-5
: Sequence 5, Application US/08709912
: Patent No. 5759840
: GENERAL INFORMATION:
: APPLICANT: Sung Dr., Wing L
: APPLICANT: Yaguchi Dr., Kazuhiko
: APPLICANT: Ishikawa Dr., Kazuhiko
: TITLE OF INVENTION: Modification of xylanase to improve
: TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
: TITLE OF INVENTION: Thermostability
: NUMBER OF SEQUENCES: 54
: CORRESPONDENCE ADDRESS:
: ADDRESS: Fitzpatrick, Cella, Harper, and Scinto
: STREET: 277 Park Ave.
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10172-0194
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/709,912
: FILING DATE: 09-SEP-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Olsen M., Warren E
: REGISTRATION NUMBER: 27290
: REFERENCE/DOCKET NUMBER: 1039, 2000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 758-2400
: TELEFAX: (212) 758-2982
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 185 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
: ORGANISM: Bacillus subtilus
: PUBLICATION INFORMATION:
: AUTHORS: Parce, M.G.
: AUTHORS: Bourbonnais, R
: AUTHORS: Desrochers, M
: AUTHORS: Jurasek, L
: AUTHORS: Yaguchi, M
: JOURNAL: Arch. Microbiol.

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: July 1, 2003, 11:49:34 ; Search time 49 Seconds

(without alignments)
425.161 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045
Sequence: 1 OTIQPGTGYNMGYFYSYMND.....YQIVAVEGYFSSGSASITVS 190Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA.*
1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686.6	65.7	313	US-10-213-990-72	Sequence 72, Appl
2	677.5	64.8	234	US-10-213-990-69	Sequence 69, Appl
3	671.3	64.2	221	US-10-213-990-66	Sequence 66, Appl
4	647.9	62.0	223	US-10-299-393-2	Sequence 2, Appl
5	647.8	62.0	217	US-09-790-070A-11	Sequence 11, Appl
6	635.9	60.9	225	US-09-467-368-2	Sequence 2, Appl
7	597.5	57.2	344	US-09-770-621-2	Sequence 2, Appl
8	481.9	46.1	133	US-09-790-070A-10	Sequence 10, Appl
9	475.5	45.5	221	US-09-909-207-3	Sequence 3, Appl
10	475.5	45.5	248	US-09-909-207-6	Sequence 6, Appl
11	437	41.8	185	US-09-970-616-2	Sequence 2, Appl
12	177	16.9	84	US-09-790-070A-9	Sequence 9, Appl
13	153.7	14.9	776	US-09-833-435A-7	Sequence 7, Appl
14	153.7	14.7	776	US-09-833-435A-4	Sequence 4, Appl
15	143.8	13.8	726	US-10-155-400-7	Sequence 12, Appl
16	143	13.7	659	US-10-090-624-12	Sequence 12, Appl
17	142.2	13.6	878	US-09-912-020-364	Sequence 364, App
18	140.2	13.4	1436	US-10-080-505-13	Sequence 13, Appl
19	139	13.3	729	US-09-815-242-10132	Sequence 10132, A

20	138.7	13.3	1974	9	US-09-895-913A-12	Sequence 12, Appl
21	137.7	13.2	943	9	US-09-996-634-131	Sequence 131, App
22	137.7	13.2	943	9	US-09-997-181-131	Sequence 131, App
23	137.7	13.2	943	9	US-09-997-182-131	Sequence 131, App
24	136.3	13.0	793	10	US-09-881-752A-362	Sequence 362, App
25	135.7	13.0	957	9	US-10-155-400-1	Sequence 1, Appl
26	135.4	13.0	719	9	US-10-234-266-2	Sequence 2, Appl
27	134.8	12.9	956	9	US-10-121-032-63	Sequence 63, Appl
28	134.8	12.9	956	9	US-10-093-037-63	Sequence 63, Appl
29	133.6	12.8	1781	9	US-09-995-749A-2	Sequence 2, Appl
30	133	12.7	553	10	US-09-888-224-2	Sequence 2, Appl
31	132.9	12.7	400	9	US-09-797-464A-4	Sequence 4, Appl
32	132.7	12.7	1043	9	US-09-917-384-6	Sequence 6, Appl
33	132.7	12.7	1043	9	US-09-917-383-6	Sequence 6, Appl
34	132.2	12.7	1477	9	US-10-092-880-4	Sequence 4, Appl
35	131.9	12.6	700	10	US-09-841-132-345	Sequence 345, App
36	131.8	12.6	522	12	US-10-090-624-4	Sequence 4, Appl
37	131.8	12.6	654	12	US-10-090-624-16	Sequence 16, Appl
38	131.2	12.6	742	10	US-09-815-242-4989	Sequence 4989, Ap
39	131.2	12.6	742	10	US-09-815-242-10634	Sequence 10634, A
40	130.9	12.5	639	10	US-09-782-906-2	Sequence 2, Appl
41	130.9	12.5	639	10	US-09-782-906-3	Sequence 3, Appl
42	130.9	12.5	639	10	US-09-782-906-4	Sequence 4, Appl
43	130.9	12.5	639	10	US-09-782-906-5	Sequence 5, Appl
44	130.8	12.5	1325	10	US-09-741-669-304	Sequence 304, App
45	130.4	12.5	925	9	US-09-924-097-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-213-990-72
; Sequence 72, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 313
; TYPE: PRF
; ORGANISM: Aspergillus
US-10-213-990-72

Query Match 65.7%; Score 686.6; DB 9; Length 313;
Best Local Similarity 64.2%; Pred. No. 1.4e-25;
Matches 124; Conservative 29; Mismatches 36; Indels 4; Gaps 3;

QY	1	OTIQRG-TCYNNNGYFYSYNDHCGVYTTNGGCGFSYVMS--NSGNFVGKGNQPGTKN 57
		11 : : : : : : : : :
DB	32	OTITTSOTCTNNGYFYSEFTNGAGSVYTNAGAGEVSYTNAMQNGDFCGKGNMPSGDH 91
		11 : : : : : : : : :
QY	58	KVINFSGSYNPNGNSTLYSGWSRNPLLEYIVENFGTYNPSTGATKJGEVYSDSDSYDI 117
		11 : : : : : : : : :
DB	92	D-TTSSGSNPNCGMAYLSYGCTTNPFLVYITLLENYGSINPSSGNTHKCTVSDSDSTDI 150
		11 : : : : : : : : :
QY	118	YTFQRYNDPSITGTATFYQYWSVRNRHSSGSVNTANHEFNAWQGLTGLTNDYOIVAVE 177
		11 : : : : : : : : :
DB	151	YHQQVQNPISVIGTATFNQYWSIRONKRSSGVTVTANHRKAWASLGMNLGTHNYOIVSTE 210
		11 : : : : : : : : :
QY	178	GYFSSGSASITVS 190
		11 : : : : : : : : :
DB	211	GYESSGTSTIVS 223
		11 : : : : : : : : :

RESULT 2
US-10-213-990-69
; Sequence 69, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ. ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-69

Query Match 64.8%; Score 677.5; DB 9; Length 234;
Best Local Similarity 63.3%; Pred. No. 2.3e-25;
Matches 119; Conservative 25; Mismatches 39; Indels 5; Gaps 1;

QY 7 TGYNNGFYFSYWNDDGCVTYTNGPGOFVSNMNSGNEFVGKMOPTK-----NKVIN 61
DB 46 TGNMNGYYSFMTDGGDVTYTGAGGSYSVNRNNGNFGGKMGNSARIALSTTN 105
QY 62 FSGSYNPNNGNSYLSVYGWSNPLIEYIVENFGTYNPSTGATKLGVTSDGSYYDIYRQ 121
DB 106 YGGSFNPNSGNGYLAIVGWTNPLIEYIVESYCTYNGSGCTRGVNTDGGTYNITAV 165
QY 122 RVNQPSTIGATYQYWSVARNHRSSGSVNTANHFNAAOGLTLGTMQYIYAVEGYS 181
DB 166 RYNAPSEGTGKPTQYWSVRSKRTGTYMANHFNAHSLGTHNYQIYAVEGYOS 225
QY 182 SGSASITV 189
DB 226 SGSASITV 233

RESULT 3
US-10-213-990-66
; Sequence 66, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ. ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-66

Query Match 64.2%; Score 671.3; DB 9; Length 221;
Best Local Similarity 59.4%; Pred. No. 4.2e-25;
Matches 120; Conservative 27; Mismatches 38; Indels 17; Gaps 2;

QY 5 PG-----TGYNNGFYFSYWNDDGCVTYTNGPGOFVSNMNSGNEFVGK 48
DB 21 PGSEQYVELAKROLTSSGTGTNGNGYYSFMTDGGDVTYTGAGGSYSVNRNNGNFGGKMGNSARIALSTTN 80

QY 49 KGWOPCTKKNKVIFFSGSYNPNNGNSYLSVYGWSNPLIEYIVENFGTYNPSTGATKLGCV 108
DB 81 KGMNPAE-KAVYSSQMTSGNGYLSVYGWTSPLVEYIVESYCTYNGSGCTRGVNTDGGTYNITAV 139
QY 109 TSDGSYYDIYRQYWSVARNHRSSGSVNTANHFNAAOGLTLGCT 168
DB 140 ESDGATYNLYKTRTAPNPSIOGTATPDQYWSVRSKRTGTYMANHFNAHSLGTHNYQIYAVEGYOS 199
QY 169 MDYQIYAVEGYPSSGSASITVS 190
DB 200 FDMYIVATEGYOSGSASITVS 221

RESULT 4
US-10-299-393-2
; Sequence 2, Application US/10299393
; Publication No. US20030108642A1
; GENERAL INFORMATION:
; APPLICANT: Sabatier, Alain
; APPLICANT: Haigh, Neville Marshall
; APPLICANT: Fish, Neville Paterson
; TITLE OF INVENTION: PENICILLIUM FUNICULOSUM STRAIN USEFUL
; FILE REFERENCE: A32917-PCT-USA-1 (072667.0183)
; CURRENT APPLICATION NUMBER: US/10/299,393
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 09/462,246
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: EPO 9801161.5
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ. ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Penicillium funiculosum
US-10-299-393-2

Query Match 62.0%; Score 647.9; DB 9; Length 223;
Best Local Similarity 61.4%; Pred. No. 5.7e-24;
Matches 113; Conservative 29; Mismatches 41; Indels 1; Gaps 1;

QY 7 TGYNNGFYFSYWNDDGCVTYTNGPGOFVSNMNSGNEFVGKMOPTKKNKVINFSGSY 66
DB 41 TGNMNGYYSFMTNNGGCVTYTNGDNGEYSVTWVDCGDTSGKGNPANA-QYVTSGEF 99
QY 67 NPNNGSYLSVYGWSNPLIEYIVENFGTYNPSTGATKLGVTSDGSYYDIYRQYVNOP 126
DB 100 NPSGNAYLAIVGWTTPDVEYIVLESYCTYNPSSGLTSLGOVYSDGCTYDIYSTORVNOP 159
QY 127 SIIGTATFYQYWSVARNHRSSGSVNTANHFNAAOGLTLGTMQYIYAVEGYS 186
DB 160 STEGSTFQYWSVRSKRTGTYMANHFNAHSLGTHNYQIYAVEGYOS 219
QY 187 ITVS 190
DB 220 ITVS 223

RESULT 5
US-09-790-070A-11
; Sequence 11, Application US/09790070A
; Publication No. US20030053999A1
; GENERAL INFORMATION:
; APPLICANT: Jomiaux, Jean-Luc
; APPLICANT: Davurin, Thierry
; TITLE OF INVENTION: ENZYME WITH XYLANASE ACTIVITY
; FILE REFERENCE: VANM199.001AUS
; CURRENT APPLICATION NUMBER: US/09/790,070A
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: EP 00870028.8
; PRIOR FILING DATE: 2000-02-21

SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-770-621-2

Query Match 57.2%; Score 597.5; DB 10; Length 344;
Best Local Similarity 53.5%; Pred. No. 3e-21;
Matches 106; Conservative 35; Mismatches 42; Indels 15; Gaps 4;

QY 5 PGT-----GYNNGYFYSYNNDDHGVYTYNGPGQFVSVMNSGNGFVGKGMQ 52
DB 38 PGTAAHDTTITONQOTGYDNGYFSEWTDAPGTVSMTLHSGSYSTSMRNTGNFVACKGWS 97
QY 53 PGTKNVINFSGNSYLSVYGMNRNPLIEYIVENFGYNPSTGATKIGEYTSQG 112
DB 98 TGR-RTVYVNSFNFGYLTGVTNRNPLIEYIVESWGYRP-TGYK-GVYTTDG 154
QY 113 SYVDIYRTQVNOPSIIGTATFYQVSVRRNHRSSGVNTANHFNAQAQGLTGTMDYO 172
DB 155 GTYDIYETRWYVNSIEGTRTFQGFVSVQOKRTSGTITIGNHFDAMARAGMLGSHDYQ 214
QY 173 YVAVEGYFSSGSASTVS 190
DB 215 IMATEGYQSSGSSTVSIS 232

RESULT 8

US-09-790-070A-10
Sequence 10, Application US/09790070A
Publication No. US20030053999A1
GENERAL INFORMATION:
APPLICANT: Jonaux, Jean-Luc
APPLICANT: Dauvin, Thierry
TITLE OF INVENTION: ENZYME WITH XYLANASE ACTIVITY
FILE REFERENCE: VANM199.001AUS
CURRENT APPLICATION NUMBER: US/09/790,070A
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: EP 00870028.8
PRIOR FILING DATE: 2000-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 133
TYPE: PRT
ORGANISM: Penicillium griseofulvum
US-09-790-070A-10

Query Match 46.1%; Score 481.9; DB 9; Length 133;
Best Local Similarity 67.4%; Pred. No. 2.3e-16;
Matches 89; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 60 INFSGSYNPNNGNSYLSVYGMNRNPLIEYIVENFGYNPSTGATKIGEYTSQSVYDIYR 119
DB 2 INFSGFNFSGANAYLAIVMTKGPLVEYIYMEYNGGSMTEFGYTSQSVYDIYK 61
QY 120 TORVNOPSIIGTATFYQVSVRRNHRSSGVNTANHFNAQAQGLTGTMDYOIAVYEG 178
DB 62 HTQVNOPSIISDSSTFDQYWSIRNRKRSCTVTTGNHFNAKALGMLGSHDYQVNTBG 121
QY 179 YFSSGSASTVS 190
DB 122 YOSSGSASTVS 133

RESULT 9

US-09-909-207-3
Sequence 3, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
ERIC DE BUYL

PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced lt.
DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-909-207-3
Query Match 45.5%; Score 475.5; DB 10; Length 221;
Best Local Similarity 45.4%; Pred. No. 1e-15;
Matches 93; Conservative 29; Mismatches 58; Indels 25; Gaps 4;

QY 8 GYNNGYFYSYNDHGVYTYNGPGQFVSVMNSGNGFVGKGMQ-----WPGTKNK 58
DB 9 GNHDDYDEYFMRKDSGSGTMIILNHGTFSAQNNVNNILFRKGRFNETQHQVG--NM 66
QY 59 VNFSGSYNPNNGNSYLSVYGMNRNPLIEYIVENFGYNPSTGATKIGEYTSQSVYDIY 118
DB 67 SINIGANFOPNNAFLCYGTVDPPLVEYIVDSWGNMRP-PGATPKGTVYDGGTYDIY 125
QY 119 RTQVNOPSIIGTATFYQVSVRRNHRSSGVNTANHFNAQAQGLTGTMDYOIAVYEG 178
DB 126 ETLRVNOPSIKIGIAFYQVSVRRNHRSSGVNTANHFNAQAQGLTGTMDYOIAVYEG 185
QY 179 YFSSGSASTVS 190
DB 186 YOSSGSANYSNLTIRINGNPLSTIS 210

RESULT 10

US-09-909-207-6
Sequence 6, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced lt.


```

; LENGTH: 84
; TYPE: PRT
; ORGANISM: Penicillium griseofulvum
US-09-790-070A-9

```

Query Match	16.98;	Score 177;	DB 9;	Length 84;
Best Local Similarity	58.38;	Pred. NO. 0.046;		
Matches 28; Conservative	6;	Mismatches 14;	Indels 0;	Gaps 0;

Oy 8 GYNNGYFYSYWNDGHHGVTTNTCPGGQFSVNMWSNSGLPFGVGKGWQPCT 55
 | | | | : : : : | : | | | : : | | | :
Db 35 GTNCGYFYSFWTNGGGSVSYNNGAQQYSVNMKNCQSFTSGKGMATGS 82

```

RESULT 13
US-09-833-435A-7
Sequence 7, US00200081670A1
Patent No. US20020081670A1
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 5629.200-US
CURRENT APPLICATION NUMBER: US/09/833.435A
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 09/346,237
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/094,353
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 7
LENGTH: 776
TYPE: PRT
ORGANISM: Pseudomonas species SMP1
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(776)
OTHER INFORMATION: Isoamylase
US-09-833-435A-7

```

Query Match	14.9%;	Score 155.3;	DB 10;	Length 776;
Best Local Similarity	10.9%;	Pred. No. 18;		
Matches 74; Conservative	26;	Mismatches 60;	Indels 517;	Gaps 18;

OY	13	YEFSTYNDHG--GVTYTNPGGQ-----	FEVSNMS	42
OY	59	YLS--AGVGQESATYTLSPAGSGWAVTPVSSIKACITGAVYYGYRANGPMDEYA		115
OY	43	GNEFVGKGWQPG-----TKNKVI-----		60
OY	116	SNW--GKGSQAGFVSDVDANGDRENPKLLLDLPAGEVSDPLPNSNGNVFASGASR		173
OY	61	NFSGSYNPMG-----		70
OY	174	TTDSGIAPKGVVLVPSTQSTGCTPKRAKQDVIYEVHVGFTQDTSIPAQRYGGA		233
OY	71	NSYL-----		74
OY	234	GLKASTLASLGVTAVEFLPVOETONDANDVYVNSDANONTWGYMTENTFSPDRRAYNKA		293
OY	75	-----SVYGSRNLIIEY--		88
OY	294	AGGTAEFQAMVQAFHNAGIKVYMDVYVNHHTAEGGTWTSDDPTATIIYSMGDLNTTYE		353
OY	89	-----IVENFGTYN-----		97
OY	354	LTSQNDYFYDNTGIGANFTYNTVAQNLIVDSLAYMANTMGVDGFRFLASVLGNSCLNG		413
OY	98	-----PSTGAR-----		103
OY	414	AYTASAPNCNGGYNEDADSNVAINRLRETFYRPAAGSGLDLAEPMIAIGNSYQLG		473

```

QY 104 -----KLEGVSDGSVYIYTORVNO-----123
Db 474 GFPQGSSENNGLERDRLROAONELCSMT-----IYVQDANDESSGNLFQSSGRSPW 520
QY 126 -----PSLITATFYQY-----137
Db 527 NSINPFDVHDGMTLKDVYSCNGANNQSOAMPYGPBGDGTSTYNSWDQGSAGTGAAYDQR 566
QY 138 -----MSV-----140
Db 587 AARTGMAFEMLSAGTPTLMQGDPEYLRITLQCCNNAINLDSANMLTYSHTTQDSNFTYFAQ 646
QY 141 -----RRNH-----RSSGSV-----NTANHFNMAAOGLTLGTMZY 171
Db 647 RLIAEFKRAHPALRPSSWYSGSOLTYPQSGAIVADSNYNNNTSNVAIAVMGPELGDNS 706
QY 172 QIVAVEGYFSSGSAST 188
Db 707 IYVAYNGM-----SSVY 719

```

```

US-09-833-435A-4
US-09-833-435A-4
Sequence 4, Application US/09833435A
Patent No. US20020081670A1
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 5629.200-US
CURRENT APPLICATION NUMBER: US/09/833,435A
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 09/346,237
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/094,353
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PstSD for Windows Version 3.0
SEQ ID NO. 4
LENGTH: 776
TYPE: PPT
ORGANISM: Pseudomonas amyloclavata
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1) - (776)
OTHER INFORMATION: Isoamylase
US-09-833-435A-4

```

Query Match	14.7%	Score 153.7;	DB 10;	Length 776;
Best Local Similarity	11.0%;	Pred. No. 21;		
Matches	74;	Conservative	29;	Mismatches 64;
				Indels 503;
				Gaps 19

[illegible]

Db 354 LITSGNOYFYDNTGICANENTYNTVAONLIVDSLAWANTMGVDFRDLASVLGNSCLNG 413
QY 98 -----PSGCAT----- 103
Db 414 AVTASAPNCPNGYNFADADSNAVAINRLREFTVPAAGSGLDLFAEPMAIGNSYOLG 473
QY 104 -----KLGEBV----- 109
Db 474 GFRPGMSEWNGLFRRSLQAQNELGSMITIVYIQDANDSGSSNLFOSSGRPSNINFID 533
QY 110 -SDG-SYVDIYRTQRYNQ-----PSIIGTATFYQY----- 137
Db 534 VHDGHTLKDYSCNGANNNSQAMPYGPSPDGGTSTNYSWDQGSAGTGAIVDQRAARTGMA 593
QY 138 -----MSV-----RR 142
Db 594 FEMLSAGTPMLMGDEYLTFTLOCCNNNAVNLDSANMLTYSWTTDOSNFTYFAQRLIAFERK 653
QY 143 NH-----RSSGSV-----NTANHEFMAAOGLTLCGTMDOYQIVAVEG 178
Db 654 AHPALRPSSWYSGSOLTYWQPSGAVADSNTYMNNTSNALAYAINGPSLGDNSIYYAIVNG 713
QY 179 YFSSGSASIT 188
Db 714 W-----SSSVT 719

RESULT 15

US-10-155-400-7
; Sequence 7, Application US/10155400
; Publication No. US20030108988A1
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: ADNEY, WILLIAM S.
; APPLICANT: VINZANT, TODD B.
; APPLICANT: HIMMEL, MICHAEL E.
; TITLE OF INVENTION: THERMAL TOLERANT AVICELASE FROM ACIDOTHERMUS
; FILE REFERENCE: NREL 01-36A
; CURRENT APPLICATION NUMBER: US/10/155,400
; CURRENT FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 726
; TYPE: prt
; ORGANISM: Aspergillus aculeatus
US-10-155-400-7

Query Match 13.8%; Score 143.8; DB 9; Length 726;
Best Local Similarity 12.3%; Pred. No. 57;
Matches 72; Conservative 27; Mismatches 73; Indels 412; Gaps 21;

QY 5 PGTGY-----NNGYFYSYWMDGHG-----GVYTT 28
Db 123 PGRGGERLAVDPKNKNSILYFCARGHGILMKSTVDGATWSNVTSTWTCTYFQDSSSTYT 182
QY 29 NCPGGOFSYVNM-----SNSGN-----FVG-----GKGN----- 51
Db 183 SDPVG-----IAWVTFPSTSGSSGSATPRIFGVADAGKSVFKSEDAAGATWAMVSGEPQGF 239
QY 52 -----QPGTKNKYINFSGSYNP----- 68
Db 240 LPHKGVLSPEEKTLYISTANGAGPYDGTNGTVHKNTISGVTWDISPSLASTYGYGGL 299
QY 69 -----NGNSYLSYVGMSPNPLEY----- 88
Db 300 SVDLOVPGTLWVAALNCMMPPDELLFRSTDSGATNSPIMEMNGSPSINITYSIDISNAPWI 359
QY 89 -----IVEN----- 92
Db 360 QDTTSDQFPVREVGMMVEALAIIDPDSNHLTYGTLTYGCHDLTNWDSKHNVTKSLAV 419

QY 93 -----FGYVNPSTGATKLGEBVTSDSGVY-----DIYRQRY-----NOP 126
Db 420 GIEEMAVUGLITTPGGPALLSAVDDGCFYHSDLDAPNQAHTPTTYCTWGIDYAGNKP 479
QY 127 SII----- 129
Db 480 SNIVSGASDDYPTLALSNGSTWYADYASTGTGTGAVALSADGDTVLLMSSTSGALV 539
QY 130 -----GTAT-----FYQYWSVRNRHSSGSV-----NTANHE----- 156
Db 540 SKSQGTPLAVSSLPSCAVIASDKSDNTVEY-----GGSAGAIYVSKMTATSTFKTVS 591
QY 157 -----NANAQ-----QGLTLG----- 167
Db 592 LGSSTTVNAIRHPSIADQVMASTDGKGLMHSSTDVGSTFTQIGSGVTAGMSEFGKASSTG 651
QY 168 -----TMD-----YOIVAVEGY-FSSGSASI 187
Db 652 SYVVIYGFFTIDGAGLFRKSEDAAGTNMQVYISDASHGFGSGSANV 695

RESULT 16

US-10-090-624-12
; Sequence 12, Application US/10090624
; Patent No. US20020132335A1
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: SHIMOJO, Tomoko
; APPLICANT: ASADA, Kiyoza
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
; FILE REFERENCE: TAKAKURA-6
; CURRENT APPLICATION NUMBER: US/10/090,624
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/445,472
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 151969/1997
; PRIOR FILING DATE: 1997-06-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 659
; TYPE: prt
; ORGANISM: Thermococcus celer
US-10-090-624-12

Query Match 13.7%; Score 143; DB 12; Length 659;
Best Local Similarity 12.2%; Pred. No. 53;
Matches 67; Conservative 22; Mismatches 50; Indels 410; Gaps 18;

QY 2 TTPGTGYN-----NCGYFYSYWMDGHG-----GVY 26
Db 149 TWVNSLGYDGSVVVAIVDTGIDANHPDLKKGIVGMAYDANCRSTPYDDOGHTHVAGIV 208
QY 27 YTNG-----PGGQF-----SVNM----- 39
Db 209 ACTGSVNSOYIGVABGARKLVGVKVLGADSGSVSTIAGVDMVYONKOKYGIIVNLISLG 268
QY 40 -----SNSG----- 43
Db 269 SSQSSDGTDSLQAQVNMAMDAGIYVCAAGNSGPMITYVGSFAASKVITYGAVDSNDNI 328
QY 44 -----NEVGGKG 50
Db 329 ASESRCPTADGRLKPEVAVPCVDIILAPRASGTSMTGPIINDYYTKASGTSMTATPHVSGV 388
QY 51 -----WPGTKNKY-----INF 62
Db 389 ALIIQAHPSWTP--DKVKTALIIETADIVAPKEIADIAYGAGRVNVYKAIKYDDYAKLTF 445
QY 63 SGS-----YNPNGN-----SYLSYVGWGRN 82

```
Db 446 TGSVADKGSATHTEDVSGATFTATLYWDTSDDIDLYDPNGNEVDYATAYGF 502
      83 PLEIYIVENFGYNNP----- 98
Db 503 -----EKVGYNPNPAGTATVKKVVSYGKANYQVDVSDGSLSGCGNPNPNPNP 554
      99 -----STGATKL-GEVTSDSGSVDI----- 117
Db 555 TPTTDTQTFGVSNDYWDTSDFTFMNVNSGATKITGDLTFDTSYNDLDLYDPNGNLYD 614
      118 -----YRTQRYNOSIITATFTFYQVSVRRNHRSSGSVNTANHMAOQGLTGTMD 170
Db 615 RSTSSNSYEHEYANPA-PGTWTFLYV-----AYS-----TYGWAD 649
      171 YQIYAVEGY 179
      650 YOLKAVVYI 658
```

```
RESULT 17
US-09-912-020-364
; Sequence 364, Application US/09912020
; Patent No. US20020045592A1
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Frawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; FILE REFERENCE: ELITRA.001DVI
; CURRENT APPLICATION NUMBER: US/09/912.020
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/492,709
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/117,405
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 364
; LENGTH: 878
; TYPE: PRT
; ORGANISM: E. coli
US-09-912-020-364
```

```
Query Match 13.6%; Score 142.2; DB 10; Length 878;
Best Local Similarity 16.2%; Pred. No. 92;
Matches 51; Conservative 20; Mismatches 46; Indels 198; Gaps 12;

QY 1 QTIQPGTGY-----NNGFTYSTWMDGHGCVTYTNGPG----- 32
      71 QELPQGT-YRVDIYLNNGYMAT-----RDVTFNTSDSEQIYPCCLTRQALSMGINTAS 123
      33 -----GQFSYVMSNSGTFYVGKG-----WQPGTK 56
Db 124 VAGMNLADDACVPLTTMWDATAHLDVGQRLNLTPQAFMSNRARGIYPPELMDPGIN 183
      57 NKVINFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSTGATKLGEVTSDSQVYD 116
      184 AGLLN-----YNFSGNS-----VQN----- 198
QY 117 IYRTQRYNOSIITGATFTFYQ-----WSVRRNHRSSGSVNTANHFN 157
      199 -----RIGGSHVAYLYMLQSGNLIGAWRLRDNNTWYSNDSRSSGSKNMKQHIN 247
QY 158 AMAOQ-----LTGTMDYQIVAVEGY----- 179
      248 TWLERDIITPLRSRLTUG-----DGYTQGDIFDGINFGAQLASDNDMLPDQGRFA 298
```

```
QY 180 -----FSSGSASITV 189
      299 PVIHGIARGTAYVTI 313
Db

RESULT 18
US-10-080-505-13
; Sequence 13, Application US/10080505
; Publication No. US20030073166A1
; GENERAL INFORMATION:
; APPLICANT: St. Geme, Joseph W.
; TITLE OF INVENTION: HAEMOPHILUS ADHERENCE AND PENETRATION PROTEINS
; FILE REFERENCE: A-59941-1/PFT/DCF/DHR
; CURRENT APPLICATION NUMBER: US/10/080,505
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 08/296,791
; PRIOR FILING DATE: 1994-10-25
; PRIOR APPLICATION NUMBER: US 09/839,996
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 1436
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-080-505-13
```

```
Query Match 13.4%; Score 140.2; DB 9; Length 1436;
Best Local Similarity 9.5%; Pred. No. 2,3e+02;
Matches 70; Conservative 30; Mismatches 52; Indels 588; Gaps 22;
```

```
QY 1 QTIQPGTYNNGY-----FYSYW--NDGHGCVTYTN- 29
      269 QTSNPFSGAGNGQLIRKNMFIDNVVEDLPTFLEPRNSNGHISFTSNNGTGTVTQTN 328
      30 ----- 29
Db 329 KVSMPQFKVRYVQLFNEALKEKDEPVYAAGVNAKPRLNKKNITFGDGTGLTIEN 388
      30 -----GFGQGP-----SYNMSNSGTFV-----GKG----- 50
Db 389 NINOGAGGLYFEGCNFTVSSENNATWOGAGVHGEDSTVYKVGVEHRLSKIGKGLAI 448
      51 ----- 50
Db 449 QAKGENLGSIVDGKVIILDDQADENNOKOAKREVCIGSRATVOLNSADQVDPNNITYG 508
      51 -----WQPGTKNV--INF 62
Db 509 FRGRLDLNGHSLTFKRIQNTDEGAMIVNHNTQVANITITGNEISITAPSKNNKINIKLDY 568
      63 SG--SYNPNNGNSYLSVYGMSRNPLEYIYVENFG-----TNPST----- 100
      569 SKELIAYN-----GW-----FGETDENKHKGRNLILYKPTTEDRTLL 605
      101 -GATKL-GEVTSDSGS-----VDIYRTQRYNOSIIG-----TATF 134
      606 SCGTNLKAKNTQGGGLTGVSGRTPHAYN-----HLNRENELGRPGGEVYIDDDMITRIF 660
      135 ----YQY-----MSVRRNHR----- 146
      661 KAENFQIKGSAVAVSRNVSISIEGNTWVSNNANAAFCGVNQNQNTICTRSDWGTGLTCKTV 720
      147 ----- 150
      721 DLDTKVINSLPTTQINGSLNLTDNATVINIGLAKLNGVTLINHSQFTLSNNATQOTGNI 780
      151 NTAHNFNA----- 161
      781 QLSNHNATVDNANLNGVNLTDLSAQSILKNSHFSHQIOGDKCTTYTLENATWTMPSDAT 840
      162 -GGLT----- 166
```

Db 841 LONLTLNLTSTVLNSAYSASANNAPRRSRLETTPTSAEHRFNTLTVNGKLSGCTFO 900
167 -----
QY 167 -----
Db 901 FTSSLEGYKSKDKLSNDAEGDYTLNRTGKEPEALEQLLVESKDNKPLSDKIKETLE 960
167 -----GTMDYOIVAVEGYF 180
QY 167 -----
Db 961 NDHVDAGALRYKLVKNNGEF 980

RESULT 19
US-09-815-242-10132
; Sequence 10132, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for windows Version 4.0
; SEQ ID NO 10132
; LENGTH: 729
; TYPE: PRF
; ORGANISM: Escherichia coli
US-09-815-242-10132
Query Match 13.3%; Score 139; DB 10; Length 729;
Best Local Similarity 14.1%; Pred. No. 98;
Matches 73; Conservative 20; Mismatches 70; Indels 353; Gaps 19;
QY 8 GYNN-----CYEYS-----YNN-DG- 21
Db 227 GTGNDSDWLDRYNSEKTFEFGIVADLDGLTSLAGYEYORIDVNSPTWNGLPBWMFTDS 286
22 -----HGV-----TYT 28
Db 287 SMSYDARSTAPDMAYNDKINKVEMTLKQOFADTQATLNMATHSEVEDSKMYVDATV 346
29 NCGGCGFSVWMSNSG---NFVGGKGQPOCTKNKV-----INFGSGY 66
Db 347 NNADGMLVGPYSNYGPGFDYVGGTGWNNG-KRKVDALDLFADGSYELFGROHLMFGSGY 405
67 NNNGNSYLSVYG-----WSKNPLIE----- 86
Db 406 SKONNRYTSSMANIPFDELGSFYNNNGNFPOTDMSQSLAQQDDTHMKSLYATRTVLAD 465
87 -----YIVENFGTYNPST----- 100

Db 466 PLHLIGARYTNMRYDTLTYSMEXNHTTPEYAGLVEDINDNMSTYASTSIFQPNDRDSS 525
101 -----
QY 101 -----
Db 526 GRYLAPITGNMYELKSDMNSRLTTLTAIFRIEDDVAOSTGPPIDSGNGETAYKAVD 585
101 -----GATK-----LGE 107
QY 108 VTSDGSV-----YDIYRORVNOPG--IIGATFYQYWSVRRNHRSSGSYVTANH 155
Db 646 LTVGGVNMQRVYTDVTPYGTFRAGQGSYALVDFTRYQ---VTKNFSLOGNVN--NL 700
QY 156 FNAMAQOGLTGTMDYOIVAVEG---YESSGSASIT 188
701 FDK-----TYD---TNVEGSIVGTPRNFST 724

RESULT 20
US-09-895-913A-12
; Sequence 12, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides In t
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FASTSEQ for windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1974
; TYPE: PRF
; ORGANISM: Helicobacter pylori
US-09-895-913A-12
Query Match 13.3%; Score 138.7; DB 9; Length 1974;
Best Local Similarity 12.1%; Pred. No. 5e+02;
Matches 67; Conservative 34; Mismatches 78; Indels 373; Gaps 17;
QY 4 QPGTGNNNGYFYSYND-----GHGCVYTN-GPGGGS---YMSNSG----- 43
Db 342 QOTALENASSLSFYNSVANFNNGTTAFNGVSTLNLNPAQVSEFNQVNNANVTFFYGLP 401
44 -----NFVGGKGQPOCT-----KNKVINFGSG----- 64
Db 402 LFGKTPDFGNSARLINFKNKTNFNQATLNLRAKHINHINQGVSTFKONSTMLAESSQAS 461
65 -----SYNPNNGSYLSYGWS-RNPLLEYIVENFGTYNPSTGATKLGCVTSDG- 112
Db 462 FNAKVEGETNFNLNNSSLNFGNSVFNAPVSFY-----ANHSQISFTKLATFNSDAS 515
113 -----
QY 516 FDLNNSTLNFOSVLNGLNGLNGSNLAINAKGNFSFGKGLNLSTYMLFGDKKT 575
113 SYVDIYTORVN-----
QY 576 SVYDVLQAGNIDGLMKNNGYEKIRFYGIQIDKADYSFDNGVHSWRFNPLNLTETITETL 635
125 -----QPSIIG-----TATFYQWS-----V 140
Db 636 HNNRLKVOISONGVSNKMFNLAPSLDYOKNPYNETENSYYTSDKVGTYVLTLSNKG 695

Query Match	13.2%	Score 137.7;	DB.9;	Length 943;
Best Local Similarity	25.6%	Pred. No. 1.7e+02;		
Matches	58;	Conservative 42;	Indels 113;	Gaps 16;
Y	3	IOPCTGYNNGYFVS-----YWNDSHGCVTYTNGPG-----GQFVSNNNS	42	

Db 279 LNSGTG-NIGLFNSGTGNGVIGNSGTGMMGIGNSGNSYNTGFGNGDANTGFFNNGIANT 337
OY 43 GNFVGKMGQMGCTKNNKVINP-SCSYNPNNGSYLSTYGGSRNPLIEYIVENPGTINPSTG 101
Db 338 G-VGNAG-----NYNTGSNP-GNSNTGCG-----MMGOYN--TG 368
OY 102 ATKLGVEYSDGSVDYDRTQORVNQPSIGTATFYQYWSRRNHRSSGSVNT-----ANHEN 157
Db 369 YLNSGN-----YNTGLAN-----SGVNTGAPITGNFN 396
OY 158 ---AWA--QGGLTGTMDYQIVAVEGYFS-----GSAS 186
Db 397 NGFLMRGDHOGILFGS-----PGFNFSTSAPESSGFENSGAGSAS 435

RESULT 24
US-09-881-752A-362
; Sequence 362, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Gatawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 362
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-362

Query Match 13.0%; Score 136.3; DB 10; Length 793;
Best Local Similarity 11.1%; Pred. No. 1.5e+02;
Matches 59; Conservative 31; Mismatches 66; Indels 377; Gaps 16;

OY 5 PG-----TGNGCYFSYWNCH----- 22
Db 96 PGQIRDATGTGVLPKISVRGFGG-----GNGHSNTMILVNGIPYGAPEINIELAI 149
OY 23 -----GGVTYNGP-----GGQFSY-----MNSN----- 41
Db 150 FPPVTFQSVDRIDVIKGTFSVQYGPMTFGGVNITTKELPKKEWENQAAERITFWGSSSGN 209
OY 42 -----SGNFVGKMGQMGCTKNNKVINP-SCSYNPNNGSYLSTYGGSRNPLIEYIVENPGTINPSTG 101
Db 210 FVDPEKKGKPLAQTLGNQMLFNTYGRTAGMLGKHGISAQGWINGGQFRQNSPKYQNY 269
OY 63 -----SGSYNPN----- 69
Db 270 LLDVYKINATNTFKAYYQYYQYNSYHPTLSAODYANRFINERPDNDGGRAKFGIV 329
OY 70 -----GNSLYSYGMSRNLPIEYIVENPGTINP-SCSYNPNNGSYLSTYGGSRNPLIEYIVENPGTINPSTG 101
Db 330 YQNTFGDPDRKVGDFKFTTYTHDMSRDPGFSNOYQSYMSQNKILPFKKGKGISATNP 389
OY 99 STG-----ATKLGVEYSDGSV-----YDIYR- 119
Db 390 NCGCLSYSDJNSPCMQFNDNIRRSVYNAPEPLNLIYVTKGKQYFNNMGMRFLTEDLYR 449
OY 120 ----- 119
Db 450 STTRKPSMPNNGSGFDAGTSLNPNFNNTAVYASDEINFGNMGMLITPGLRYTFLNVEKK 509

OY 120 -----TORVNO-----PSIIGTA 132
Db 510 DAPPEKAGOTGKTIKDRINQNNPRAVNGYKRIKELLFENYQRSIYIPPOFSNIGSFVOTS 569
OY 133 T-FYQYWSRRNHRSSGS---VNTANHNMAAQGLTGTMDYQIVAVEGYFS 181
Db 570 TDYQFIFNV-----MEGSGRYEFENNQVSENA-----NYFVIFANNYFT 607

RESULT 25
US-10-155-400-1
; Sequence 1, Application US/10155400
; Publication No. US20030108988A1
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: ADNEY, WILLIAM S.
; APPLICANT: VINZANT, TODD B.
; APPLICANT: HIMMEL, MICHAEL E.
; TITLE OF INVENTION: THERMAL TOLERANT AVICELASE FROM ACIDOTHERMUS
; TITLE OF INVENTION: CELLULOYTICUS
; FILE REFERENCE: NREL 01-36A
; CURRENT APPLICATION NUMBER: US/10/155,400
; CURRENT FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Acidothermus cellulolyticus
; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (957)
; OTHER INFORMATION: Any amino acid
US-10-155-400-1

Query Match 13.0%; Score 135.7; DB 9; Length 957;
Best Local Similarity 9.9%; Pred. No. 2.2e+02;
Matches 75; Conservative 33; Mismatches 73; Indels 573; Gaps 22;

OY 2 TIQP-----GTGYNNGYFYST-----WN 19
Db 48 TTQPTWSNVAIGGGFVDGIVFNEGAPGILYVRTDIGMYRMDAANGRMIPLLDMVGMN 107
OY 20 D-GHCGVT-----YTN----- 29
Db 108 NMGTGVVSIADAPINTKNAVAGMTYNSWDPNDCAILRSSDQATWQITPLPKLGN 167
OY 30 -----GPGQFSYN-----WSNCFV----- 46
Db 168 MPGRGMGERLAVDPNDNDILFPGAPSGKGLMRSTDSGATWQMTNFPDVGTYIANPTDTT 227
OY 47 -----GKGMQ--PGTKNKVI 60
Db 228 GYQSDIQGVVWAFDSSSSSLGQSKTIFGVADPNPNVFWMSRDGATWQAVCAPGTGFI 287
OY 61 NFSSGSYNP-----NGNSYLSVY 77
Db 288 PHKGVDFVNVHLYIATSNTEGPDYDSSGDVKKFSVTSGTWTIRISPVSTDTANDYFGYS 347
OY 78 G-----WSR----- 81
Db 348 GLTIDRHPNTIMATQISMWPDITIFRSTGOGATWITIMDWTSYPRNSLKVLDISAP 407
OY 82 -----NP----- 83
Db 408 WLTFGVQNPVPSPKLGMDMEAMAIIDPFNSDRMLYGTATLYATNDTLTKWDSGOIHA 467
OY 84 -----LIEY- 87
Db 468 PMVGLLEETAVNDLISPPSAPLISALDLCGFTHADVYAVPSTIFTSPPVFTTGSVDYA 527
OY 88 ---YIVENFGTYNPST-----GATKLGVE--TSNGS----- 113

Db	528	ELNPSTIVRAGSFDPSPQENDRHVAFSTPDGCKNMFQSGEPGVTTGGTVAASAGSNFVW	587
		: :: :: ::	
		: :: :: ::	
Qy	114	-----YVDI-----YRQVNPQPSI--IGTATFQO-----YW	138
		: : : : : : : : : : : :	
Db	588	APDDPCQPPVYTAAGFGNSWASQGVPAANAQIQRSDVNPKTEYALNSGTFYRSTDGVTFO	647
		: : : : : : : : : : : :	
Qy	139	SVRRNHRSSGSVYNTANH-----	155
Db	648	PVAAGLPSSQAVGVMEHAPVKEGDLMLAASGLYHSTNGSSMSAITGVSSAAVNGFGK	707
		: : : : : : : : : : : :	
Qy	156	-----FNMAQO-----	161
Db	708	SAPGSSYPAVFVVGITGVTGAIVRSDDCGTTMVLINDDQHQYGMWGQALITGDHANLRVY	767
		: : : : : : : : : : : :	
Qy	162	-----QGLTGLTDNDIYVAVEGTFSSGASITVYS	190
		: : : : : : : : : : : :	
Db	768	IGTNGRKIYVGD-----CGADSGSPSPVVS	793

RESULT 26
 US-10-234-266-2
 : Sequence 2, Application US/10234266
 : Publication No. US20030059902A1
 : GENERAL INFORMATION:
 : APPLICANT: Cheriy, Joel
 : APPLICANT: Svendsen, Allan
 : APPLICANT: Andersen, Carsten
 : APPLICANT: Beier, Lars
 : APPLICANT: Frandsen, Torben
 : APPLICANT: Schaefer, Thomas
 : TITLE OF INVENTION: Amylolytic Enzyme Variants
 : FILE REFERENCE: 5241.204-US
 : CURRENT APPLICATION NUMBER: US/10/224,266
 : CURRENT FILING DATE: 2002-09-04
 : PRIOR APPLICATION NUMBER: US/09/645,707
 : PRIOR FILING DATE: 2000-08-24
 : NUMBER OF SEQ ID NOS: 31
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 2
 : LENGTH: 719
 : TYPE: PR1
 : ORGANISM: *Bacillus* sp.
 : US-10-234-266-2

Query Match	13.08;	Score 135.4;	DB 9;	Length 719;
Best Local Similarity	12.28;	Pred. No. 1.4e+02;		
Matches 76; Conservative	26;	Mismatches 57;	Indels 466;	Gaps 26

```

OY      8 GYNNGYFYSYV-----NCH-----22
           ||:::||
Db      116 GTDNTGTHGYWTRDFKQIEHGFNMWTFDTLVNDAHQNGIKVIYDFVPNNSTPEKANDST 175
           ||:::||
OY      23 ---GCVTTTNGP-----GCGFSYWS-----40
           ||:::||
Db      176 FAEGGALYNNNGTYMGNYFDDATKGYFHANNGIS--NMDDRYEAWKNFTDPAGESLADLSQ 234
           ||:::||
OY      41 -----NSG-----NFVGGK--GWQ 52
           ||:::||
Db      235 ENGTINQVLTDAVQVLAHGADGLRLIDAVKHNPSGFSKSLADKLQYKKDLFIYGEWGGDD 294
           ||:::||
OY      53 PGCKN-----KYINF-----GSY-----NPGNST-----73
           ||:::||
Db      295 PGTAHLEKRYVYANNSGVNVLDLNTFVIRNVEGTFQOTMYDLNMVNGTGNEYKKENL 354
           ||:::||
OY      74 -----LSV-----76
           ||:::||
Db      355 ITPIDHDSRFLSVSNKANLHQLAFILTRSGTPSIYGTGEQYMGAGNDPYNRGMPRA 414
           ||:::||
OY      77 -----YG-----MSRNPLEY-----87
           ||:::||
Db      415 FDTTTTAFKEVSTLAGLRNNNAALQYGTGTQRMWINDVYIYERKFFNDVVLAINRNTOS 474
           ||:::||

```

```

QY      88 -YVENPGT-----YNPSTGATKL 105
      | : |
      | : |
Db      475 SYISGLQTLALPNGSTADYLSGLGNGISVNSGVSASFTLAPGAVSWQISISAPQI 533
      | : |
      | : |
QY      106 GE-----VTSDSGVDIYRTQRYNOPSIIIGATF-----134
      | : |
      | : |
Db      535 GSAVPNMGIGPNVNTIDGKFGF--FTQ-----GTVTFGGVATVKSMTSNRIEYVP 584
      | : |
      | : |
QY      135 -----YQY-----137
      | : |
      | : |
Db      585 NMAAGLTDVKKVYAGGVSSNLSYISNILSGTQISVETVKSAPETNIGDKITYLTGNIPELGN 644
      | : |
      | : |
QY      138 WSVRRNHRHSSGVNTAN-----HFNAM-----AQOGLTL-----GTMDYQIVAV 176
      | : |
      | : |
Db      645 WST-----DTSGAVNNAOGPLAPNPVDMVEYFSPAGKTIOKFEFIKRAODGIOE---- 686
      | : |
      | : |
QY      177 EGFSSGS-----ASITVS 190
      | : |
      | : |
Db      697 -----GGSNHVATTPTGATGNTITVT 716

```

Db 697 -----NGSNHVATTPTGATGNTVT 716

```
RESULT 27
US-10-121-032-63
; Sequence 63, Application US/10121032
```

Patent NO. US20020155550A1
GENERAL INFORMATION:

APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES

NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:

ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600

CITY: San Diego
STATE: CA

COUNTRY: USA
ZIP: 92121

```

;
;      COMPUTER READABLE FORM:
;
MEDIUM TYPE: Diskette

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95

```

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

```

COMMUNITY DEVELOPMENT DISTRICT
 APPLICATION NUMBER: US/10/121,032
 FILING DATE: 08-Apr-2002

```

      ;
      CLASSIFICATION: <unknown>
      EXPIRATION DATE: 09 Apr 2002
      ;
      DPOB ADDITION DATA.
```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/134,078
 FILING DATE: 12-MAR-2009

FILING DATE: 13-AUG-1998
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-SEP-1997

FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916

ATTORNEY/AGENT INFORMATION:
FILING DATE: 06-DEC-1996

NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465

```

; INFORMATION FOR SEQ ID NO: 63:
;
; SEQUENCE CHARACTERISTICS:

```

```

;
; LENGTH: 956 amino acids
;
; TYPE: amino acid

```

TOPOLOGY: linear
MOLECULE TYPE: protein

```

PROGRAM      : prog0001
:
:
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO. 63.
:
:

```

US-10-121-032-63

Query Match	12.98;	Score 134.8;	DB 9;	Length 956;
Best Local Similarity	13.18;	Pred. No. 2.4e+02;		
Matches 63; Conservative	26;	Mismatches 70;	Indels 322;	Gaps 16

QY 6 GTGYNNGYFY--YWN-----DG- 21
| | | | |
Db 414 GLDYNNKYLISIEGDYWNKIDIEFKTGSKGIVLDSNGSKLNLVYHDIGEAIHLRDS 473
QY 22 -----HGVYTYTG--PG-----32
| | | | |
Db 474 SNNSIDCCTIYNGRTKPGEGELYGSDKGQHDYERACNNNTIENCTVGPVNTAEGVD 533
QY 33 -----GQFSVWMSNSGNFVG-----47
| | | | |
Db 534 VKEGTMTTIRNCVFSAEIGISGENSSDAFIDLKGAIGFYRNFTFNDGSEVINTGVDFLD 593
QY 48 -GKMGPGTKNKVYNFSGSYN-----67
| | | | |
Db 594 RGTGFNTGFRNAT--FENTYNLGSRAEISTARKKQSPROTHWDMIRNPNSVDPISD 651
QY 68 -----PNGN-----SYLSVYGSNRNPLEIYIVNF-----93
| | | | |
Db 652 GTENLVNKKFCPDWNIIEPCNPVDETNQAPTISFLS-----PVNNITLVGYNLQVEVNA 704
QY 94 -----GTYNSTGATKLGCV 108
| | | | |
Db 705 TDADGTIDNVKLYIDNNLVQIINSTYKMGHSDSPNTDELNGLTGTYTLKALAT-----759
QY 109 TSDGSV-----YDIYRTQRYNQ-----PSIIGTA 132
| | | | |
Db 760 DNGCASTETQFTLVITEQSPSENCDEPTPSSTGLEDFDIKFSNVFELSGSPSLNLK 819
QY 133 TTYQYVSVRRNHHSSGSVNTANHFMAAOGGLTGLTMDYQI---VAVEGFSSGSASITV 189
| | | | |
Db 820 TFTINMNSQYNGLYQFSINTNN-----GVPDYIYNLKPKITFOFKNANPEISI 867
QY 190 S 190
Db 868 S 868

RESULT 28
US-10-093-037-63
; Sequence 63, Application US/10093037
; Publication No. US20030078397A1
; GENERAL INFORMATION:
; APPLICANT: Jay M. Short
; APPLICANT: Bylina, Edward
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Mathur, Eric J.
; APPLICANT: Lam, David E.
; FILE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
; FILE REFERENCE: 09010-024006
; CURRENT APPLICATION NUMBER: US/10/093,037
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 09/910,579
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/134,078
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 08/949,026
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/056,916
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Bankia gouldi
US-10-093-037-63

Query Match 12.9% Score 134.8; DB 9; Length 956;
Best Local Similarity 13.1%; Pred. No. 2.4e+02;
Matches 63; Conservative 26; Mismatches 70; Indels 322; Gaps 16;
QY 6 GTGYNNGYFY--YWN-----DG- 21
| | | | |

Db 414 GLDYNNKYLISIEGDYWNKIDIEFKTGSKGIVLDSNGSKLNLVYHDIGEAIHLRDS 473
QY 22 -----HGVYTYTG--PG-----32
| | | | |
Db 474 SNNSIDCCTIYNGRTKPGEGELYGSDKGQHDYERACNNNTIENCTVGPVNTAEGVD 533
QY 33 -----GQFSVWMSNSGNFVG-----47
| | | | |
Db 534 VKEGTMTTIRNCVFSAEIGISGENSSDAFIDLKGAIGFYRNFTFNDGSEVINTGVDFLD 593
QY 48 -GKMGPGTKNKVYNFSGSYN-----67
| | | | |
Db 594 RGTGFNTGFRNAT--FENTYNLGSRAEISTARKKQSPROTHWDMIRNPNSVDPISD 651
QY 68 -----PNGN-----SYLSVYGSNRNPLEIYIVNF-----93
| | | | |
Db 652 GTENLVNKKFCPDWNIIEPCNPVDETNQAPTISFLS-----PVNNITLVGYNLQVEVNA 704
QY 94 -----GTYNSTGATKLGCV 108
| | | | |
Db 705 TDADGTIDNVKLYIDNNLVQIINSTYKMGHSDSPNTDELNGLTGTYTLKALAT-----759
QY 109 TSDGSV-----YDIYRTQRYNQ-----PSIIGTA 132
| | | | |
Db 760 DNGCASTETQFTLVITEQSPSENCDEPTPSSTGLEDFDIKFSNVFELSGSPSLNLK 819
QY 133 TTYQYVSVRRNHHSSGSVNTANHFMAAOGGLTGLTMDYQI---VAVEGFSSGSASITV 189
| | | | |
Db 820 TFTINMNSQYNGLYQFSINTNN-----GVPDYIYNLKPKITFOFKNANPEISI 867
QY 190 S 190
Db 868 S 868

RESULT 29
US-09-995-749A-2
; Sequence 2, Application US/09995749A
; Patent No. US20020155568A1
; GENERAL INFORMATION:
; APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
; APPLICANT: DIJKHUIZEN, LUBBERT
; APPLICANT: RAHAOUI, HAKIM
; APPLICANT: LEER, ROBERT-JAN
; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
; FILE REFERENCE: B043388-CIP
; CURRENT APPLICATION NUMBER: US/09/995,749A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 09/604,957
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: EPO 00201871.1
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1781
; TYPE: PRT
; ORGANISM: Lactobacillus reuteri
US-09-995-749A-2

Query Match 12.8% Score 133.6; DB 9; Length 1781;
Best Local Similarity 14.2%; Pred. No. 7.4e+02;
Matches 80; Conservative 20; Mismatches 80; Indels 384; Gaps 22;
QY 4 QPCTGYNNGYFY-----SYWNGHGVTV-----TNGP-----G 32
| | | | |
Db 235 OPTFDKNNYAYLDTFEYKNGELHATGMATNSAINVNHFFVILFDOTNCKEVARQREYRE 294
QY 33 GQ-----FSY-----NNSNSGNFVGK-----49
| | | | |
Db 295 GQSRPDYAKVYPOVYGAANSFVNTFNISLDYTHQYVLSRYSNSDNGGDVNTYWFNP 354
QY 50 -----GW-----51

Db 355 QSIAPANOSNOGYLDSFDISKNGEVTYTGMMNATDLSLQNNHYVLLFPDQTAGKQYASAKA 414
Oy 52 -----OPGTRKKYIN-FSGSYNPNGN----- 71
Db 415 DLISRPVAKAYPYKATATNGEFKYTFKVNMLQPOHOSVSVRSFADENGNDKRRHTDY 474
Oy 72 -----SYLSVYGM-----SRNPLIEYIYVENFG-----T 95
Db 475 WFSPIYLNQASINIDITMTNSGLHAGWMSDMSINFTTPYAIILNNGKEVTROKMSLT 534
Oy 96 YNPSTGAT-----KL-----GEVTSDSGYD 116
Db 535 ARPVAAYPSPLYSNVAVSFGDTTIKLTNDYOALNGOLVLLRFSKADGPNPSCGDNVTYTD 594
Oy 117 IY-----RTQRYNPS 127
Db 595 QFSKNYATTGNGFQYKYNQOVEFSGMHAATNOSNDKDSOMITVLNKGKVKROLVNDTK 654
Oy 128 IIGTATFYQVWSVRN-----HRSSGSYNT 152
Db 655 -EGAAAGF-----NRNDYKYNPAIENSSMSGFOGIIITLPYTKNENYQVLRHRSNDYKT 707
Oy 153 --AAHFMAA-----QOGL-TLCTNDYOIVANEG----- 178
Db 708 GEGNYVDWSELMPVKDSFOKNGPLKQFGLQTINGOQYIIDPTTGPRKNFLLQSGNNW 767
Oy 179 -YFSSGS-----ASTYVS 190
Db 768 IYFSDPTGCVTNALELOFAKCTVS 791

RESULT 30
US-09-888-224-2

Sequence 2, Application US/09888224
Patent No. US20020120118A1
GENERAL INFORMATION:
APPLICANT: Lam, D. et al.
TITLE OF INVENTION: Endoglucanases
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/888,224
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/430,669
FILING DATE: 28-Oct-1999
APPLICATION NUMBER: US/08/651,572
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Charles J. Herron
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 331400-48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: Unknown

TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-888-224-2

Query Match 12.7%; Score 133; DB 10; Length 553;
Best Local Similarity 11.8%; Pred. No. 1.2e+02;
Matches 58; Conservative 25; Mismatches 60; Indels 350; Gaps 18;

Oy 1 OTIDPCT----- 7
Db 59 QSVKPGTWPTAIDYAKNPDLOGLDSDVOIMEKIIKAGDLGIFLLDYHRIGCNFIEPLWY 118
Oy 8 -----GYNGY-----FYSYV-----NDHGCG-----YTNNGPG-----GQFSV 37
Db 119 TDSFSEDYINTWVEVAGRFKYNVIGADLKNRPHSSPARAAYTQSGATMGMINAT 178
Oy 38 NMSNSGN-----FY-----GKGWQPGT----- 55
Db 179 DWNLAERIGRAILEVAPQWVIFVEGQFTTPEIDGRYKMGHNMGMGMLGVKRYVNL 238
Oy 56 -KNRVI-----NFSGSY 66
Db 239 PRDKVVISPOYVGSEVIDQPIFDPEGEPDNLPEIMYHNHGYVLDLGYPVIGIEFGKY 298
Oy 67 NPNG-----NSYLSVYGMARNPLIEYIYVENFG----- 94
Db 299 GHGDDPRDVTWQNKIIDMIMQNKFCDFPYSWMN-----NSGDTGGLKDDWTTIME 350
Oy 95 -----TYNST----- 100
Db 351 DKYNNLRKLMDSGSMATAPSPRTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 410
Oy 101 -----GATKIGEVTS DG 112
Db 411 TTTTPSNVNPPEIYVNLPTSSQYEGTSEYVYCDGTQCASSWYKAPNLMGVYKIGMATMDP 470
Oy 113 SVY---DIYRTQRYVNPISITATFYQVWSVRNHRSSGSYNTANHFN----- 157
Db 471 NVMGMEDVYKT---AQDIDGTG-----STKMEIR-NGVLKYNLMNINMHPRKYNTMAY 519
Oy 158 -----ANAOQ 162
Db 520 PEVIYGAKPWGNQ 532

RESULT 31

US-09-797-464A-4
Sequence 4, Application US/09797464A
Publication No. US20030022807A1
GENERAL INFORMATION:
APPLICANT: Wiltling, Reinhard
APPLICANT: Bjornvad, Mads Eskelund
APPLICANT: Kauppinen, Markus Sakari
APPLICANT: Schultein, Martin
TITLE OF INVENTION: Family 5 xyloglucanases
FILE REFERENCE: 6073.200-US
CURRENT APPLICATION NUMBER: US/09/797,464A
CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 400
TYPE: PRT
ORGANISM: Paenibacillus sp.
US-09-797-464A-4

Query Match 12.7%; Score 132.9; DB 9; Length 400;
Best Local Similarity 18.8%; Pred. No. 73;
Matches 68; Conservative 23; Mismatches 50; Indels 221; Gaps 22;
Oy 6 GTGYNNG-----YF----- 14
Db 48 GAGWNLGNQLEATVNGVPSFTAMGNPVVTPDLIKKYKAGFKTIRIPSVYLNHIGAPNY 107


```
OY 15 -----YSYWNDS-----HGGVITYNGPGQFVSNWNSGNEVG--GKG 50
DB 108 TINAAMLNRVQTVVOYAY-NEGLYVYINIHGD-GVNSIPGGLVNGSQAIAIKREKYKV 165
OY 51 WOP-GTK-----NKVINESGSY-NPN-----GNS- 72
DB 166 WOIAITKFSNNYNERLIFESMNEV--FDGNGYGNPNNAAYANLNAYOIEVDIVROTGGNNN 223
OY 73 --YLSVYCGMSRNPILLEYIVENEG-----TYNP-STGATK 104
DB 224 ARMLIIPGMMNTN--ID-YTVGNVGFALPTDHRSSAIPSSOKRIMISAHYSPMDFAGEE 280
OY 105 LGEVTSDG-----SVYDIYRTORVNOPSIIG----- 130
DB 281 NGNITQWGAATNPSSKSTWGEDYLNQFMSMDKFTVQ--GYPVIGESPSIDKTAID 338
OY 131 -----TATFYQ-----YMSVRN-----HRSSGSVNTANHFMAAQO 162
DB 339 STNNVYRQAYAKAVATATAKYGAVPVYWMNGHNGHGFALFMRSNNTV-----TQO 389
OY 163 GL 164
DB 390 GT 391

RESULT 32
US-09-917-384-6
; Sequence 6, Application US/09917384
; Publication No. US20030096342A1
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: ADNEY, WILLIAM S.
; APPLICANT: VINZANT, TODD B.
; APPLICANT: DECKER, STEPHEN R.
; APPLICANT: HIMMEL, MICHAEL E.
; TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
; FILE REFERENCE: 40170.6US01
; CURRENT APPLICATION NUMBER: US/09/917,384
; CURRENT FILING DATE: 2001-07-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1043
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Segment of
; OTHER INFORMATION: GuXA
US-09-917-384-6

Query Match 12.7%; Score 132.7; DB 9; Length 1043;
Best Local Similarity 9.3%; Pred. No. 3.5e+02;
Matches 70; Conservative 40; Mismatches 69; Indels 573; Gaps 22;

OY 9 YNNGYFYS-----YWNDSHG--VITYNGPG-----QFSVNM----- 39
DB 219 YEOGLEIALTKLHAIPNYITYMDAAHSGWLGWPNNAAGVVOEVOKVLNASTGVNGIDGFV 278
OY 40 SNSGNF-----VGSK----- 49
DB 279 TNTANYTPLKEPFMTATQOVGQPVESANFYQWNPDIIDEADYAVDLSRLVAGFPSSIG 338
OY 50 -----GW-----OPGTNKVYNFSGS-----YNPN----- 70
DB 339 MLIDLRLNCGWGPNEPTGPSTATDVNTFVNOGKIDLRQHRGLMCQNGAGLGQPPQASPT 398
OY 71 ---NSYLSYCGMSRNP----- 83
DB 399 DEPNALHDAIYVVIKPGGESDGTSAASDPYTGKKSDBMCDPTTYSYGLTNALPMSPIAG 458
OY 84 -----LI 85
```

```
DB 459 QWEPAQDQVLANARPAVSGGLKVOYKNNDSAPCDNOIKPGLQLVNTGSSSDLSLTVYV 518
OY 86 EYV-----IYENFTYMPST-----CAT 103
DB 519 RYWFTRDGGSSSTLYVNCMAANGCGNIRASFSGSVNPAFPAJDTYLOLSFTGCTLAAGST 578
OY 104 KLGEV-----TSDGSV----- 114
DB 579 --GEIQNKVNSKSDMSNFTETNDYSYGTNTTTPQDMTKVYVYVNGVLVMGTEDVTPSPVPG 636
OY 115 -----YDIYRT-QRYNOPSI-----IGATFYQY--- 137
DB 637 LVVTGVSQSSVSLAMNASTDQVVAHVYVYRNGVLVGOPTVTSFTDGLAAGTAVTYVA 696
OY 138 ----- 137
DB 697 AVDAAGNTSAPSTPVDCPPGPNQNGVTSVODGEYRVQTNEMNNSAQOCLJTINTATGAMTV 756
OY 138 ----- 137
DB 757 STANFSGTGACAPATYPSYIKGCHWGNCTTKNVGMPDIQISQISAVTSKSTTOVSSGAYD 816
OY 138 -----WSYRRNRHRS- 147
DB 817 VAYDIWNTSTPTTGQPNQTEIMILNSRGVQPGSQATGVTVAAGHTWNNVWQGOQTSW 876
OY 148 -----GSVYTNH-----FNAAQGLTIGTMDY 171
DB 877 KIISVYLPFGATISLNDKAIFFADAARGSIINTSDYLDYVAGFEIW--QCGOGLGNSNF 935
OY 172 QIVAVEG-----YFSSGSASITVS 190
DB 936 SVSVTSGVACRATYVVSNDWGSQFTATYTVT 967

RESULT 33
US-09-917-383-6
; Sequence 6, Application US/09917383
; Publication No. US20030104522A1
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: ADNEY, WILLIAM S.
; APPLICANT: VINZANT, TODD B.
; APPLICANT: DECKER, STEPHEN R.
; APPLICANT: HIMMEL, MICHAEL E.
; TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
; FILE REFERENCE: 40170.6US01
; CURRENT APPLICATION NUMBER: US/09/917,383
; CURRENT FILING DATE: 2001-07-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1043
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Segment of
; OTHER INFORMATION: GuXA
US-09-917-383-6

Query Match 12.7%; Score 132.7; DB 9; Length 1043;
Best Local Similarity 9.3%; Pred. No. 3.5e+02;
Matches 70; Conservative 40; Mismatches 69; Indels 573; Gaps 22;

OY 9 YNNGYFYS-----YWNDSHG--VITYNGPG-----QFSVNM----- 39
DB 219 YEOGLEIALTKLHAIPNYITYMDAAHSGWLGWPNNAAGVVOEVOKVLNASTGVNGIDGFV 278
OY 40 SNSGNF-----VGSK----- 49
DB 279 TNTANYTPLKEPFMTATQOVGQPVESANFYQWNPDIIDEADYAVDLSRLVAGFPSSIG 338
```

QY 50 -----GW-----QPGTKNKVIFSGS-----YNPNG-----70
DB 339 MLIDTLRNGMGCGNEPRTGPSTADVTNFVNSKIDLRHRLGRLCNGNAGLGGPPOASPT 338
QY 71 ---NSYLSVYWGSRNP-----83
DB 399 DFNNAHLDAVYWIKPGEESDGTSAASDPPTGKKSDPKDPTTYTTSYCVLTALPNSPIAG 458
QY 84 -----L1 85
DB 459 QMPPAEFDOLVANAAPVAVSGGLKVOYKKNDSAPGDNQIKPGQLVNTGSSVLDSTVY 518
QY 86 EYV-----IVENFGTYNPST-----GAT 103
DB 519 RYMFTRDGGSTLVYNGDMAAMCGCINRASFGSVNPTPTADYTLQSLFTGTLLAAGST 578
QY 104 KLEGV-----TSDGSV-----114
DB 579 --GEIQNRVKSMDMSNETETNDYSYGTNTTFODMTKVYVYVNGVLWGTEDVTPPSVPTG 636
QY 115 -----YDIYRT-QRVNOPSI-----IGTATFYQY---137
DB 637 LVYTVSGSSVSLAMNASTDNGVANHVRNGVLGQPTVTSFTDTGLAAGTAYTYVA 696
QY 138 -----137
DB 697 AVDAAGTSAPTVPDCTPGPNONGVTSVDGEYRVQTNEMNSSAQOCLINTATGAMTV 756
QY 138 -----137
DB 757 STANFSGGTGABATYPSIYKGGWGNCTKNVGMPIQISQISAVTSMSTTGVSSGAYD 816
QY 138 -----WSVRNRHRS-147
DB 817 VADITNSTPTTTGGOPNGTEIMWLSRGCVPPFGSQTATGTVAGHTNNVYMGQQTSM 876
QY 148 -----GSVNTANH-----FNMAOQGLTLGTM DY 171
DB 877 KIISVLTGATISINDLKAFADAARGLSLTSDVLLDVEAGFEIW-QGGGGLGSNSF 935
QY 172 QIYAVEG-----YFSSGSASTVS 190
DB 936 SVSVTSGGVACRATYVYVNSDMGSGGTATYVT 967

RESULT 34
US-10-092-880-4
Sequence 4, Application US/10092880
Patent No. US20020164354A1
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS OF NON-TYPEABLE
FILE REFERENCE: HAEMOPHILUS
CURRENT APPLICATION NUMBER: US/10/092.880
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 09/155,614
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 08/617,697
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: PCT/US97/04707
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 1477
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-10-092-880-4

Query Match 12.78; Score 132.2; DB 9; Length 1477;
Best Local Similarity 11.58; Pred. No. 6.4e+02;

Matches 55; Conservative 35; Mismatches 59; Indels 328; Gaps 13;
QY 1 QTIQPGTYNGGTFYVWMDHG-----GVYTT-----28
DB 646 QTTTRKNT-----SYWQTSHDHWNVSALNLETGANFTFKYISSNSKGLTTOYRSSA 697
QY 29 -----NGPGQFS-----36
DB 698 GVNFGVNGMSFNLKEGAKVNFKLPNENMNTSKPLPIFLANITATGGGSVFEDITAN 757
QY 37 -----VMSNSGNF-----45
DB 758 HSGRGAELKMSLEINISNGANFTLNSHVRGDDAFKINKDLTINATNSFSLRQTKDDPYDG 817
QY 46 -----YGGKW-----QPGTKNKYI 60
DB 818 YARNAINSTYNIISILCGAVTLGGQSSSITGNTITEKANVTLNANNAPOQNDIRVI 877
QY 61 -----NFGSYNPNGNSYLSYVGS 80
DB 878 KLGSLVNGSLSLTGENADIKNLTISEATFEGKTRDRLNITGNFTNNGTAELNI-----933
QY 81 RNPLEYIYVENFGTYNPSTGATKLGCVTSQSVYDIYRTQRYNOPSITGTATFYQYWSV 140
DB 934 -----TOGVYKLGNTVNDGDL-NITTHAKNRHSIIIGDII-----968
QY 141 RRNHRSSGVNTANHFN-----157
DB 969 -----NKKSLINTDSNNDAEIQTGNIISQREKMLTSSDKINITKOITTKKIGDEDDSS 1024
QY 158 -AWAQGLTLGTM DYI---VAVEGY-----FSSGSASTVS 190
DB 1025 DATSNANLTIKTTELKLTEDLSISGFNAKEITAKKDRDLTIGNSNGNSGAEKTYVT 1081

RESULT 35
US-09-841-132-345
Sequence 345, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhacta, Ajay
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 345
LENGTH: 700
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-841-132-345

Query Match 12.68; Score 131.9; DB 10; Length 700;
Best Local Similarity 13.98; Pred. No. 2e+02;
Matches 73; Conservative 19; Mismatches 43; Indels 391; Gaps 23;
QY 1 QTIQPGTY-----NNGFYSYWMDHGIGVTV 27
DB 15 QLSQGGQGFAPIGQAMAIAGQIKLPTVHIPTAFILGLVDNNG-----59
QY 28 TNG-----PGGFSVNVN---39
DB 60 -NGARVQRYVGSAPASLSIGTGDVITAVDGA PINSATAMADALNCHHGDAVSYTWQTK 118
QY 40 ---SNSGNFVGGG-----WQP-GT-----58
DB 119 SGTTRGTGNVTLAEGPAEFRCRYPHWRPLGTIVFSSSELEHNSYIPQNALHNGTLVKE 178
QY 59 -----VINP-----62

```
Db 179 KTELHVFSEFOEGSKLIMEPGAVLSNONIANGALAINGLITLIDSSMGTPOAGEIFSPPE 238
      ||:|
QY 63 -----SGS-----YNPNG 70
Db 239 LKIVATTSASGSGSVSSIPNPKRISAAPVSGSAATPTPMSENKVELTGLDITLIDPMG 298
      |||
QY 71 NSYLSVYGWSRNPLIEYIVENFGYNPSTGA-----TKLGEVTSDSGVYDI-----117
      ||:|
Db 299 NRY-----ONPMLGSDLDVPLKLPNTISDVQYVDITLISGLDF 336
      ||:|
QY 118 ----YRTQRYNOPSIIGTATF-----YQWVSV--RRNHRSSGSV-----150
      ||:|
Db 337 POKGY-----MGTTLDSNPQGTGLQARWTFEDTYRRWYIIPRDNHFYANSILGSQ 386
      ||:|
QY 151 -----NTAN-----HFNAN-----AOGGLTL-----GTMDYQI 173
      ||:|
Db 387 NSMIVYKQGLINMLNNAHFDDIAINNFVSGVGTFLAQQGTPLSEFYSYSGTS-----442
      ||:|
QY 174 VAVE-----GYFSSGS-----AST 187
      ||:|
Db 443 VALDAKPRQDFILGAFAFSKIVCKTKAIKKMHNFFHKSEYSYQASV 488
      ||:|
```

```
RESULT 36
US-10-090-624-4
: Sequence 4, Application US/10090624
: Patent No. US20020132335A1
: GENERAL INFORMATION:
: APPLICANT: TAKAKURA, Hikaru
: APPLICANT: MORISHITA, Mio
: APPLICANT: SHIMOJO, Tomoko
: APPLICANT: ASADA, Kiyozo
: APPLICANT: KATO, Ikunoshi
: TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
: FILE REFERENCE: TAKAKURA-6
: CURRENT APPLICATION NUMBER: US/10/090,624
: PRIOR FILING DATE: 2002-03-06
: PRIOR APPLICATION NUMBER: 09/445,472
: PRIOR FILING DATE: 1999-12-06
: PRIOR APPLICATION NUMBER: 151969/1997
: PRIOR FILING DATE: 1997-06-10
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 522
: TYPE: prt
: ORGANISM: Pyrococcus furiosus
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (428)..(428)
: OTHER INFORMATION: xaa at position 428 is Gly or Val.
US-10-090-624-4
```

```
Query Match 12.6%; Score 131.8; DB 12; Length 522;
Best Local Similarity 13.5%; Pred. No. 1.3e+02;
Matches 65; Conservative 19; Mismatches 46; Indels 352; Gaps 19;
```

```
QY 8 GYN-----NGYFYSYWNNDGHGCVTY-----27
      ||:|
Db 22 GYDGSITIGIIDTGIDASHPDLQGVIGWDFVNGRSYPRYDDHGHG--THVASIAGTG 79
      ||:|
QY 28 --TNG-----PGGQFS-----VNMS-----40
      ||:|
Db 80 AASNGKYKGMAPGAKLAGIKVLGADSGSISITIKVEWAVDNKKYGIKVINLSLGSSQ 139
      ||:|
QY 41 -----NSG-----43
      ||:|
Db 140 SSDGTDLALSQAVNAAMDAGLVVVVAAGNSGPKMYTTIGSPAASKVITVGAVDKYDVTSEF 199
      ||:|
QY 44 -----NFGGKGW-----QPGTK-----56
      ||:|
Db 200 SSRGPTADGRLEPEYVAPGNMTIIAARASGTSMGQPIINDYYTAAPGTSMTAPHVAGIAALL 259
      ||:|
```

```
QY 57 -----NRKYNF-----62
      ||:|
Db 260 LOAHPSWTFDKVKTALLETADIYKPEIADIYAGACRVNAVKAJINDNAAKLVTGYVAN 319
      ||:|
QY 63 -----SGS-----YNPNGN-----SYLSVYGWSRNPLIEY 88
      ||:|
Db 320 KCSQTHQFVISAQSEFVATLTYMDNANSDLDLXYLPNGNQVDYSTAYYGF-----370
      ||:|
QY 89 IYENFGTYNPSG-----ATKLGEVTSDSGVYDIKRTQRYNOPPS-----11GT 131
      ||:|
Db 371 --EKVGYNPTGTGTWIKVYSYSGSANYQVDVSDGL-----SQGSSPSQPEPTVDA 423
      ||:|
QY 132 ATF-----YQWVSVRNHRSSGSVNTANFNMAAQGLTGTMQYQIVAVEGYFSSGSAS 186
      ||:|
Db 424 KTFQXSDHYT-----DKSDIFTYKTVN-----SGATK 450
      ||:|
QY 187 IT 188
      ||:|
Db 451 IT 452
      ||:|
```

```
RESULT 37
US-10-090-624-16
: Sequence 16, Application US/10090624
: Patent No. US20020132335A1
: GENERAL INFORMATION:
: APPLICANT: TAKAKURA, Hikaru
: APPLICANT: MORISHITA, Mio
: APPLICANT: SHIMOJO, Tomoko
: APPLICANT: ASADA, Kiyozo
: APPLICANT: KATO, Ikunoshi
: TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
: FILE REFERENCE: TAKAKURA-6
: CURRENT APPLICATION NUMBER: US/10/090,624
: PRIOR FILING DATE: 2002-03-06
: PRIOR APPLICATION NUMBER: 09/445,472
: PRIOR FILING DATE: 1999-12-06
: PRIOR APPLICATION NUMBER: 151969/1997
: PRIOR FILING DATE: 1997-06-10
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 16
: LENGTH: 654
: TYPE: prt
: ORGANISM: Pyrococcus furiosus
US-10-090-624-16
```

```
Query Match 12.6%; Score 131.8; DB 12; Length 654;
Best Local Similarity 13.5%; Pred. No. 1.8e+02;
Matches 65; Conservative 19; Mismatches 46; Indels 352; Gaps 19;
```

```
QY 8 GYN-----NGYFYSYWNNDGHGCVTY-----27
      ||:|
Db 154 GYDGSITIGIIDTGIDASHPDLQGVIGWDFVNGRSYPRYDDHGHG--THVASIAGTG 211
      ||:|
QY 28 --TNG-----PGGQFS-----VNMS-----40
      ||:|
Db 212 AASNGKYKGMAPGAKLAGIKVLGADSGSISITIKVEWAVDNKKYGIKVINLSLGSSQ 271
      ||:|
QY 41 -----NSG-----43
      ||:|
Db 272 SSDGTDLALSQAVNAAMDAGLVVVVAAGNSGPKMYTTIGSPAASKVITVGAVDKYDVTSEF 331
      ||:|
QY 44 -----NFGGKGW-----QPGTK-----56
      ||:|
Db 332 SSRGPTADGRLEPEYVAPGNMTIIAARASGTSMGQPIINDYYTAAPGTSMTAPHVAGIAALL 391
      ||:|
QY 57 -----NRYVNF-----62
      ||:|
Db 392 LOAHPSWTFDKVKTALLETADIYKPEIADIYAGACRVNAVKAJINDNAAKLVTGYVAN 451
      ||:|
QY 63 -----SGS-----YNPNGN-----SYLSVYGWSRNPLIEY 88
      ||:|
```

```
Db 452 KGSQTHQVYSGASFVATLTYMDNANSDDLTYLDENGNOVDYSTYAYVGF----- 502
QY 89 IVENFCTYSPSTG-----ATKLGCVTSDSGVYDIYRTQVRNOPS-----ICGT 131
Db 503 --EKVGYVNTDGTMTIKVYVSGSANYOVVDVSDSL-----SOPGSSPSQPPEPTVDA 555
QY 132 ATE-----YQVMSVRNRHSSGCVNTANHFNMAAQGLTGTMDOIVAVEGYFSSGSAS 186
Db 556 KTFQGSDDHYT-----DSSDFTMTVY-----SGATK 582
QY 187 IT 188
Db 583 IT 584

RESULT 38
US-09-815-242-4989
: Sequence 4989, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4989
: LENGTH: 742
: TYPE: PRF
: ORGANISM: Enterococcus faecalis
US-09-815-242-4989

Query Match 12.6%; Score 131.2; DB 10; Length 742;
Best Local Similarity 13.7%; Pred. No. 2.4e+02;
Matches 65; Conservative 28; Mismatches 64; Indels 318; Gaps 19;

QY 7 TGYNNGYFS-----YWDG---HGGVY---TNG--- 30
Db 105 TCQNNKELYAEKKDFDDIAELAKYTKLDKKTALKYLNNGIHEDGSTOYQVEFGTCGQNI 164
QY 31 -----PGGFS-----VNMSNSGN-----FVGCGK 50
Db 165 TLETROKIEADLKKKKISGVYFNEHPARLYPNGQFASHFTGYTKANPDDEKGLVGANG 224
QY 51 -----PGGFS-----VNMSNSGN-----FVGCGK 50
Db 225 LEOYNDILSGTDGRVYFEKOIYGNALPQTVAEKKAVDGGDIYTTLDLRLONTLEDLMT 284
QY 51 -----WQ-----PGTK 56
```

```
Db 285 QVNEXYEYVSWTAMLMKAEKTGEIVAMSQRPTENPETKQGLDNGCTQNNLLVESPYEPGST 344
QY 57 NKVYNS-----GSYND-----NGNSYLS---VYGSRN- 82
Db 345 IKLETTAASMEQOQFNPNELFNRVGGIOVGDTYVNDHYTRLNGKEYLVYRQAISSWSNI 404
QY 83 -----PLIEYIVENGTGYNPSTGATKLG----- 107
Db 405 GMYKLEQKMGDEKEMLEYLKKFEGT-----STHSGLSESGAKLPGTNFVRNMSAFQCAIT 461
QY 108 -----VTSQGSVYDIYRTQVRNOPSIICTATFEYQVMSVRNRH 145
Db 462 VTNFQMKGFSALANGDSMLQPHYISKIYDKNTGKETITEPQIVGCPPIAAQ----- 512
QY 146 SSGSVNTANHFNMAAQGLT--LGTMD-----YQIVAVEGYF---SSGSASIT 188
Db 513 -----TAQQIRTYMIDTIVEDPTGYIAYDVRKVPYHAAKGTQAOIS 554

RESULT 39
US-09-815-242-10634
: Sequence 10634, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10634
: LENGTH: 742
: TYPE: PRF
: ORGANISM: Enterococcus faecalis
US-09-815-242-10634

Query Match 12.6%; Score 131.2; DB 10; Length 742;
Best Local Similarity 13.7%; Pred. No. 2.4e+02;
Matches 65; Conservative 28; Mismatches 64; Indels 318; Gaps 19;

QY 7 TGYNNGYFS-----YWDG---HGGVY---TNG--- 30
Db 105 TCQNNKELYAEKKDFDDIAELAKYTKLDKKTALKYLNNGIHEDGSTOYQVEFGTCGQNI 164
QY 31 -----PGGFS-----VNMSNSGN-----FVGCGK 50
Db 165 TLETROKIEADLKKKKISGVYFNEHPARLYPNGQFASHFTGYTKANPDDEKGLVGANG 224
QY 51 -----WQ-----PGTK 50
```

Db 225 LEQTYNDILSGDGRVFEKDIYGNALPQTVAEKKAVGDODIYTTLDSRLONTLEDLMT 284
QY 51 -----WO-----PGTK 56
Db 285 OVNKEYEVSMTAMLEAKTGEIVAMSORPTFPNETKOGCLDNGWOMLVESPEPGST 344
QY 57 NKVINFSGSYNP-----NGNSYLS--VYGMSPN- 82
Db 345 IKLFYTAASMEGCGPNPHELFNRVGIQVGDVYVNDHYTRNGKEIYLNRAISMSSNI 404
QY 83 -----PLIEYIVENFGTYNPSTGATKIGE----- 107
Db 405 GMYKLEOKMGDEKMEYLLKKEFGFT--STHSGLGESAGKLPCTNFVDRAMSAFGAIT 461
QY 108 -----VTSDSGVYDIYRTQR-----VNPSIICTATFYQWYSRRNHR 145
Db 462 VTNFQMKGFSAIANDGSMLOPHYSKIYDKNTKETITTEPQIVGTPIKAQ----- 512
QY 146 SSGSVNTANHFMAQAQGLT--LGTM-----YQIVAVEGYF--SSGSASIT 188
Db 513 -----TMOQIRTYMIDIVEDPTGYIAVDIKVPGYHVAAKTGTAOIS 554

RESULT 40
US-09-782-906-2
; Sequence 2, Application US/09782906
; Patent No. US20010051369A1
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Rittenhouse Pruss, Jennifer L.
; APPLICANT: Murphy, Dennis J.
; APPLICANT: Maffia III, Anthony M.
; APPLICANT: Bylina, Edward J.
; APPLICANT: Coleman, William J.
; TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, And Method
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: HER-0040
; CURRENT APPLICATION NUMBER: US/09/782,906
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/185,001
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Dactylium dendroides
US-09-782-906-2

Query Match 12.5%; Score 130.9; DB 10; Length 639;
Best Local Similarity 13.8%; Pred. No. 1.9e+02;
Matches 68; Conservative 34; Mismatches 68; Indels 321; Gaps 23;

QY 4 OPGTGY-----NNG---YFYSYNDGHCAGVYTTNGPGC-QFSVMSN 41
Db 155 OPGICRMGPTIDLPVPAAAAEPTSGRYLWMSYRNDAFGG-----SPGCITLTSSMDP 209
QY 42 SGNFY-----GSK-----GMQPG----- 54
Db 210 STGIYSDRTVYTKHDMFCPGISMDNGQIVYTGNDAKKTSLYDSSSDSWIPGDMQYA 269
QY 55 -----TNKVINFSGS-----YNNNGNSYLS----- 75
Db 270 RGYOSSATMSDGRVFTTIGSGMSGVFEKNGEYVSPSSKTWTSLPNAKVNPMULTADKQGLY 329
QY 76 -----VYGSRNPLIE-----YYI----- 89
Db 330 RSDNHAMLFQMKKGSVFQAGPSTAMNMYTTSGSGDYKSAKROSNRGVAPDAMCGNAVY 389
QY 90 -----VENFG--TYNPSTGATK-----LGE-----VTS 111
Db 390 DAVKGIILTFGSGSPDYQSDATTNAHITTLGEPGTSPTVTFASNGLYFAFTFHTSVVLDP 449

QY 112 GSVY-----DIYRTORVNPSSIIGTATFYQ-----YMSVR- 141
Db 450 GSTFITGGQRGICIPREDSTPVFTPEIYVPEQ-----DTFYQONNSIYRVYHSTL 500
QY 142 -----RNRHSSGSV--TNANHFNA-----WAOGLTLG-- 167
Db 501 LLPDGRVENGGGGLCGDCTTNHFDQIFTPNYLYNSNGNLATRPKITRPTSTQSVKVGRI 560
QY 168 -----IMDYOI-----YAVEGYF-- 180
Db 561 TTSDDSSISKASLIRYGTATHTVNTDORRIPLLTTLNNGNSYSFQPSDGVALLPGYMWL 620
QY 181 -----SSGSASI 187
Db 621 FVMNAGVPSV 631

RESULT 41
US-09-782-906-3
; Sequence 3, Application US/09782906
; Patent No. US20010051369A1
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Rittenhouse Pruss, Jennifer L.
; APPLICANT: Murphy, Dennis J.
; APPLICANT: Maffia III, Anthony M.
; APPLICANT: Bylina, Edward J.
; APPLICANT: Coleman, William J.
; TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, And Met
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: HER-0040
; CURRENT APPLICATION NUMBER: US/09/782,906
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/185,001
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NO. US20010051369A1el sequence
US-09-782-906-3

Query Match 12.5%; Score 130.9; DB 10; Length 639;
Best Local Similarity 13.8%; Pred. No. 1.9e+02;
Matches 68; Conservative 34; Mismatches 68; Indels 321; Gaps 23;

QY 4 OPGTGY-----NNG---YFYSYNDGHCAGVYTTNGPGC-QFSVMSN 41
Db 155 OPGICRMGPTIDLPVPAAAAEPTSGRYLWMSYRNDAFGG-----SPGCITLTSSMDP 209
QY 42 SGNFY-----GSK-----GMQPG----- 54
Db 210 STGIYSDRTVYTKHDMFCPGISMDNGQIVYTGNDAKKTSLYDSSSDSWIPGDMQYA 269
QY 55 -----TNKVINFSGS-----YNNNGNSYLS----- 75
Db 270 RGYOSSATMSDGRVFTTIGSGMSGVFEKNGEYVSPSSKTWTSLPNAKVNPMULTADKQGLY 329
QY 76 -----VYGSRNPLIE-----YYI----- 89
Db 330 RSDNHAMLFQMKKGSVFQAGPSTAMNMYTTSGSGDYKSAKROSNRGVAPDAMCGNAVY 389
QY 90 -----VENFG--TYNPSTGATK-----LGE-----VTS 111
Db 390 DAVKGIILTFGSGSPDYQSDATTNAHITTLGEPGTSPTVTFASNGLYFAFTFHTSVVLDP 449
QY 112 GSVY-----DIYRTORVNPSSIIGTATFYQ-----YMSVR- 141
Db 450 GSTFITGGQRGICIPREDSTPVFTPEIYVPEQ-----DTFYQONNSIYRVYHSTL 500

QY 142 -----RNHRSSGSV---NTANHFNA-----WAQGLTLG--- 167
| | | | |
Db 501 LLPDGVFVGGGGLCGDCTTNHFDQIIFPNLYNSNGNLATRPKTRTSTQSVKVGGR 560
QY 168 -----TMDYOI-----VAEGYF--- 180
| | | | |
Db 561 T1STDSSISKASLIRYGTATHTVNTDQRRIPLTLTNNGNSYSFQVPSDGVALPGYWML 620
QY 181 ----SSGSASI 187
| | | | |
Db 621 FVMNSAGVPSV 631

RESULT 42
US-09-782-906-4
; Sequence 4, Application US/09782906
; Patent No. US20010051369A1
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Rittenhouse Pruss, Jennifer L.
; APPLICANT: Murphy, Dennis J.
; APPLICANT: Maffia III, Anthony M.
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, And Method
; FILE REFERENCE: HER-0040
; CURRENT APPLICATION NUMBER: US/09/782,906
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/185,001
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. US20010051369A1el Sequence
US-09-782-906-4

Query Match 12.5%; Score 130.9; DB 10; Length 639;
Best Local Similarity 13.6%; Pred. No. 1.9e+02;
Matches 67; Conservative 33; Mismatches 70; Indels 321; Gaps 21;

QY 4 QPCTG-----YNNGF-----YSWN----- 19
| | | | |
Db 155 QPGLGHWGPTLPLPIPAATAIEPTSGRVLWMSSTRNDAFAGSPGILTLTSSWDPSTGIY 214
QY 20 -----DGHGCVTYTNG-----PGGQF 35
| | | | |
Db 215 SDRTVTVTKHDMFCPCISMDNGQIVVTGNDAKKTSLYDSSSDSWIPGDMQVANGYOS 274
QY 36 SVNMSNSGNFVGKGNQPGT--KNKYINFGSYNPNNGSYLS----- 75
| | | | |
Db 275 SATMSDGRVFTIGGSMGCVFEKNGEV-----YSPSKTWTSLPNKAVNPMLTADKGLY 329
QY 76 -----YVGNRNPLIE-----YYI----- 89
| | | | |
Db 330 RSDNNAHMLFGMKGSYFQAGPSTAMNMYTSGSGDVKSAGKROSNRGVAPDAMSGNAVY 389
QY 90 -----VENFG---TYNPSTGATK-----LGE-----VTSQ 111
| | | | |
Db 390 DAVKCKILTFGGSPDYODSDATTNHIIITLGEPTGSPNTVFASNGLHFAFTHTSVVLPD 449
QY 112 GSVY-----DIYRQARNQPSIICTATFYQ-----YWSVR- 141
| | | | |
Db 450 GSTFTTGGRCRGIPEEDSTPVFTPEIYVDEQ-----DIFYKONPNSIVRAVHSISL 500
QY 142 -----RNHRSSGSV---NTANHFNA-----WAQGLTLG--- 167
| | | | |
Db 501 LLPDGVFVGGGGLCGDCTTNHFDQIIFPNLYNSNGNLATRPKTRTSTQSVKVGGR 560

QY 168 -----TMDYOI-----VAEGYF--- 180
| | | | |
Db 561 T1STDSSISKASLIRYGTATHTVNTDQRRIPLTLTNNGNSYSFQVPSDGVALPGYWML 620
QY 181 ----SSGSASI 187
| | | | |
Db 621 FVMNSAGVPSV 631

RESULT 43
US-09-782-906-5
; Sequence 5, Application US/09782906
; Patent No. US20010051369A1
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Rittenhouse Pruss, Jennifer L.
; APPLICANT: Murphy, Dennis J.
; APPLICANT: Maffia III, Anthony M.
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, And Met
; FILE REFERENCE: HER-0040
; CURRENT APPLICATION NUMBER: US/09/782,906
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/185,001
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. US20010051369A1el Sequence
US-09-782-906-5

Query Match 12.5%; Score 130.9; DB 10; Length 639;
Best Local Similarity 13.8%; Pred. No. 1.9e+02;
Matches 68; Conservative 34; Mismatches 68; Indels 321; Gaps 23;

QY 4 QPCTG-----NNG-----YFYSYWNDDHGGVTYTNGPGG--QFSYVNSN 41
| | | | |
Db 155 QPGLGHWGPTLPLPIPAATAIEPTSGRVLWMSSTRNDAFGG-----SPGGLTLTSSWMP 209
QY 42 SCGNV-----GCK-----GWQPG----- 54
| | | | |
Db 210 STGIYSDRTVTVTKHDMFCPCISMDNGQIVVTGNDAKKTSLYDSSSDSWIPGDMQVA 269
QY 55 -----TKNKVINFGS-----YNPNNGSYLS----- 75
| | | | |
Db 270 RGYQSSATMSDGRVFTIGGSMGCVFEKNGEVYSPSKTWTSLPNKAVNPMLTADKGLY 329
QY 76 -----YVGNRNPLIE-----YYI----- 89
| | | | |
Db 330 RSDNNAHMLFGMKGSYFQAGPSSAMNMYTSGSGDVRSAGKROSNRGVAPDAMSGNAVY 389
QY 90 -----VENFG---TYNPSTGATK-----LGE-----VTSQ 111
| | | | |
Db 390 DAVKCKILTFGGSPDYODSDATTNHIIITLGEPTGSPNTVFASNGLHFAFTHTSVVLPD 449
QY 112 GSVY-----DIYRQARNQPSIICTATFYQ-----YWSVR- 141
| | | | |
Db 450 GSTFTTGGRCRGIPEEDSTPVFTPEIYVDEQ-----DIFYKONPNSIVRAVHSISL 500
QY 142 -----RNHRSSGSV---NTANHFNA-----WAQGLTLG--- 167
| | | | |
Db 501 LLPDGVFVGGGGLCGDCTTNHFDQIIFPNLYNSNGNLATRPKTRTSTQSVKVGGR 560
QY 168 -----TMDYOI-----VAEGYF--- 180
| | | | |
Db 561 T1STDSSISKASLIRYGTATHTVNTDQRRIPLTLTNNGNSYSFQVPSDGVALPGYWML 620

OY 181 ----SSGSASI 187
Db 621 FVMNSAGVPSV 631

RESULT 44
US-09-741-669-304
Sequence 304, Application US/09741669
Patent No. US20020022718A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allen
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for
FILE REFERENCE: ELITRA 009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 304
LENGTH: 1325
TYPE: PRF
ORGANISM: Escherichia coli
US-09-741-669-304

Query Match 12.5%; Score 130.8; DB 10; Length 1325;
Best Local Similarity 13.5%; Pred. No. 6.3e+02;
Matches 70; Conservative 27; Mismatches 68; Indels 352; Gaps 21;

OY 2 TIOPG-----TGYN-----NGVF----- 14
Db 255 TIREGLVTAENTIIIGNATIGITLVQODSVITVRLYNGIFGNGIVNISNGLINK 314
OY 15 -YS-----YWN----- 19
Db 315 EYSLVGVQDGHGVVNTDKHMHNFGLGTGEAFRIYIIGDAGDELNVSSSEKVDGIIITA 374
OY 20 -----DGHG-----GVYTTNG----- 30
Db 375 GKKEGTGNTIVKDKNSVITNLGTNLGVDGHEMNISNOGLVYNSGSSSLGYGCTGVNV 434
OY 31 ----PGGQFSV-----NMSNGNFV-----GKGWQGTGN----- 57
Db 435 SITTGGMVEVKNKVITTTIGVAGVGNLNIISDGKFEVSQNTIFLDGRKASGIGTLMDATSS 494
OY 58 -----KVINFSGSYNPNGNSYLSYG-----WS----- 80
Db 495 FDTVGINVGNFGSGIYNVNSNGATLNTGYGFIGNMSGKGINVISTDSLMLNKTSSNNO 554
OY 81 -----RNPLEY----- 88
Db 555 LLQVGLTGTGELNITTTGIVKARDQIALNDKSGDVRVDGQNSLLETFRMYVGTSGTGT 614
OY 89 -IYENFGTNPSTGATKLEGVTSDSGVYDIYRTQVNOPSI-----IGTA----- 132
Db 615 LILTNNGTLNVEGGEVYLG-----VFEPVGTGLNTIGAAGHGAADAGT 658
OY 133 -----TFYQWVSVRNRHRSQS-----VNTANH--FN 157
Db 659 TNATKVEFGIGGVF-----NHTNNSDAGVQVMDLITGDOKGVINDAGHTVFN 710
OY 158 AM-AOQGLT---GTMDYQIYAVEGFFSSGSASTVS 190
Db 711 AGNTYSGKTLVNDGLTTIASHADAGVTGMSSEVTIA 747

RESULT 45
US-09-924-097-14
Sequence 14, Application US/09924097

Patent No. US20020156240A1
GENERAL INFORMATION:
APPLICANT: TOMONO, Jun
APPLICANT: NOMURA, Yoshiko
APPLICANT: SAGAWA, Hiroaki
APPLICANT: SAKAI, Takeshi
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: ALPHA-AGARASE AND PROCESS FOR PRODUCING THE SAME
FILE REFERENCE: TOMONO-1
CURRENT APPLICATION NUMBER: US/09/924,097
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: JP00/00966
PRIOR FILING DATE: 2000-02-21
PRIOR APPLICATION NUMBER: 11-44890
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: 11-198852
PRIOR FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 925
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence of agarase 1-7
US-09-924-097-14

Query Match 12.5%; Score 130.4; DB 9; Length 925;
Best Local Similarity 8.9%; Pred. No. 3.7e+02;
Matches 76; Conservative 29; Mismatches 67; Indels 686; Gaps 22;

OY 10 NNGEFS-----YWNDSHGVTYTNNG-----PGGQFSVN----- 38
Db 39 NSCGTFADQANPITITTYNCGEALSYVACGVYVDYINTEGGDYSVEELVNGTVAASGPT 98
OY 39 -----WNSNG-----NF-----VGKQWQ----- 52
Db 99 IEMLVKENGWVWSQGVAVAPQGSMDNFPPLSPSHLVTLPAGAASIRLHAIGSNWQNLIES 158
OY 53 -----PG-----TKKKVINF----- 63
Db 159 FSLQVTPLEGASVADVVELENFINTDKDRNAIAGDSVYGFQGTNNGINFTLGDYADY 218
OY 64 -----GSYNP-----NGNSYLSV-----GWS----- 80
Db 219 HYNFASPGTYNYSIAGSTVQOIGAEIILLNCTVANSNLSATAGDDVDODFALIGDYII 278
OY 81 ----- 80
Db 279 ANAGHTTIRKVSYSANMOMNGDSITFTHISDDTNGSNQAMHLEPPVAIPESRIKSS 338
OY 81 -----RNPLEY----- 87
Db 339 WMYTPQNSNLAFGSDFGATGAFWGHMPEEDLYDSGLSNWVNOYGYRNGLDVGGE 398
OY 88 -----YIENFG-----TYNP----- 98
Db 399 FDMGFNMFLEIYVGDPTSHARTLDDOPLMSFNGHEHNGIYLNGLWLSNNSPTFVDFKSO 458
OY 99 -----STGATKLEVTSDGSVY-----DIYRTQVNOPSI- 128
Db 459 VDALLSANVSHIMFDSQTSSTKSTLDGFGGDFSTWMDAFREYMRDKYTTAELNFKGIT 518
OY 129 ----- 128
Db 519 NINAENYRFLRSRGYTHASYMAANKITSGIPLFDDFIYFNRAVLNERMAEVLDIRSI 578
OY 129 -----IGTAT----- 133
Db 579 DADIEGATTALEANGYIFDKDLTFLAGELMAGSAVADDEMPITIIISHLSAEAVDKTLY 638
OY 134 -----FYQ 136

Db 639 YFPYPMNFKDLDRNSPQMARWIAOSYANGAIFSIIPANWIGDAGVMSPGADNYRDLQ 698
137 Y-----W-----SVR-----141
Db 699 FASDNALLDGYAFKVGGLVSPMMSLDITWIDGSRLOTSTRYLIENNLNFDLIFGD 758
142 -----141
Db 759 PGKPVPTQAALDAIIVDSRKYLTDAQNLNLDANNQKVIDLNSADTAIINALKAT 818
142 -----RNHSSGS-----VTAHFHNAAOQGLTGTMDY 171
Db 819 NISVTIGNAADDITLALSRYHESNNAPYIQLNRPVNPAN-----GYTPVLSNV 870
172 QIVAVEGYFSSGSATIV 189
Db 871 KIAIPQGYFPEGITQATV 888

RESULT 46
US-10-002-309B-2
Sequence 2, Application US/10002309B
Patent No. US20020160433A1
GENERAL INFORMATION:
APPLICANT: WISCONSIN ALUMNI RESEARCH FOUNDATION
TITLE OF INVENTION: E. COLI O157:H7 C1 ESTERASE INHIBITOR-BINDING PROTEIN AND METHODS
FILE REFERENCE: 096429-9117
CURRENT APPLICATION NUMBER: US/10/002.309B
CURRENT FILING DATE: 2002-04-19
PRIORITY APPLICATION NUMBER: 60/243,675
PRIORITY FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 886
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid pO157
US-10-002-309B-2

Query Match 12.5% Score 130.3; DB 9; Length 886;
Best Local Similarity 12.1% Pred. No. 3.5e+02;
Matches 66; Conservative 31; Mismatches 72; Indels 377; Gaps 18;
1 QTI-----OPGTGYNNGYFYYSWNDS-----21
|||
Db 316 QTIPTVSRMIVNNYAPRLHLKLVMLPTGELLTMDPGNG-----HGSTMRORIGKEL 367
22 -----HGC-----VTYING 30
368 VSHGIDNANYGLNSTAGLGENSHPRVYVAQLAHNSRGNVANGIOVHGSGGCGIVTLDSF 427
31 PGQGFVSNNSNS---GNFVCG-----KGMOPGTKKNVIN-----62
428 LGNEFHEVGHANGLGHVYDGFKGVYSRAENNNSTWGMGDKKRFIPNFPYPSQTNEKSC 487
63 -----SGS-----YNPNNGNSYLSV-----77
488 LNNQCEPRFGHAFGFDAMAGSGSPSAAANRFTWTPNASSAIORFENKAVPDSRSSTGF 547
78 -----GMSRNPILI 85
548 SKWNADTOEMEPYEHTIDRAEQTASVNLSESKMAELMAEYAVVYVHMNGMWTNR---604
86 EYIIVENFGTYNASTGATKICEV-----TSDGSYV 115
605 -----IYIPTASADNNGSILITINHEAGYSYLFINGDEKVVSGYKKSFFVSDGQFW 655
116 ---DIYRTORVNOPSLI-----GTATFYQYWSV-----140
656 KENDVYDTHKARKPEQFGVPTVTLVGYDPEGLTSSYIYPAMGAVGFTYSDDSQNLSDN 715

QY 141 -----RNHSSGSVNTANHPN-----AWA 160
|||
Db 716 DCQLOVDNTRKQGLRFLRANRANTYNNKRHINVPESOPTQATLVCKNKKILDTKSLTPA 775
QY 161 OQGLTGTMDYQ-----YVAVEGYFSSGS- 184
|||
Db 776 PEGITY-TVNGQALPAKENEGCIYVNSGRYCLPVGQBSGSLPDMIVGQGEYVDSGAK 834
QY 185 ASITVS 190
Db 835 AKVLLS 840

RESULT 47
US-09-797-464A-2
Sequence 2, Application US/09797464A
Publication No. US20030022807A1
GENERAL INFORMATION:
APPLICANT: Wilting, Reinhard
APPLICANT: Bjornvad, Mads Eskelund
APPLICANT: Kauppinen, Markus Sakari
APPLICANT: Schuilein, Martin
TITLE OF INVENTION: Family 5 xyloglucanases
FILE REFERENCE: 6073,200-US
CURRENT APPLICATION NUMBER: US/09/797,464A
CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 395
TYPE: PRT
ORGANISM: Paenibacillus pabuli
US-09-797-464A-2

Query Match 12.4% Score 130.1; DB 9; Length 395;
Best Local Similarity 18.6% Pred. No. 97;
Matches 69; Conservative 21; Mismatches 51; Indels 229; Gaps 23;
6 GTGYNNG-----YF-----14
|||
Db 43 GAGMNLGNQLEAAVNGTPNETANGNPTYPELIRKKAAGFKSIRIPVSTLNNIGSAPNY 102
QY 15 -----YSWNDS-----HGVTYTNGPGQGFVSNMSNGNFVGG-----48
|||
Db 103 TINAAMLNRIQGVVDVAY-NEGLYIINIHD-CYNSVQCGMLLVN-----GGNQT 152
49 -----KGMOP-GTK-----NKVINFGSY-NPN-----69
|||
Db 153 IKKKYKVMQOLATKFSNVDRLIFESMNEV-FDCNNGPNASAYTYTNLNAVQIFVDIV 210
70 -----GNS-----YLSVGSMSRNPLEYIYVENFG-----TYN 97
|||
Db 211 ROTGNNNAKMLLVPCMNNT-ID-YTVGNGYGTLPDNYRSSAIDSSOKRIMISAHYVS 267
QY 98 P-STGATKICEVTSDC-----SVYDIYRTORVNOPSLIG---130
|||
Db 268 PMDFAGEBNGNITQMGATSTNPAKKTWGOEDLESQFMSMYKFTYQ--GYIVYIGEG 325
131 --TATFYQ-----YSVVRN-----HRSSGSYNTAN 154
|||
Db 326 SIDKTSYDSNNYRAAYAKAVTAKAKYKMPVYVDNNGHGFALPFRSNNTVTQON 385
QY 155 HFNAQAQGL 164
Db 386 IINA-IMQGN 394

RESULT 48
US-10-155-400-3
Sequence 3, Application US/10155400
Publication No. US20030108988A1
GENERAL INFORMATION:
APPLICANT: DING, SHI-YOU


```

1  APPLICANT: ADNEY, WILLIAM S.
2  APPLICANT: VINZANT, TODD B.
3  APPLICANT: HIMMEL, MICHAEL E.
4  TITLE OF INVENTION: THERMAL AVICELASE FROM ACIDOTHERMUS
5  TITLE OF INVENTION: CELLULOLYTICUS
6  FILE REFERENCE: NREL 01-36A
7  CURRENT APPLICATION NUMBER: US/10/155,400
8  CURRENT FILING DATE: 2002-10-22
9  NUMBER OF SEQ ID NOS: 7
10 SOFTWARE: PatentIn Ver. 2.1
11 SEQ ID NO 3
12     LENGTH: 740
13     TYPE: PRT
14     ORGANISM: Acidothermus cellulolyticus
15     FEATURE:
16     OTHER INFORMATION: Catalytic domain GH74
17     US-10-155-400-3

```

Query Match	12.48;	Score 130.1;	DB 9;	Length 740;
Best Local Similarity	10.68;	Pred. No. 2.7e+02;		
Matches 70;	Conservative 31;	Mismatches 68;	Indels 489;	Gaps 21

[illegible]

RESULT 49
US-10-155-400-6
; Sequence 6, Application US/10155400
; Publication No. US20030108988A1
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU

```

: APPLICANT: ADNEY, WILLIAM S.
: APPLICANT: VINZANT, TODD B.
: APPLICANT: HIMMEL, MICHAEL E.
: TITLE OF INVENTION: THERMAL TOLERANT AVICELASE FROM ACIDOTHERMUS
: TITLE OF INVENTION: CELLULOGLUCOSID
: FILE REFERENCE: NREL 01-36A
: CURRENT APPLICATION NUMBER: US/10/155,400
: CURRENT FILING DATE: 2002-10-22
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO: 6
: LENGTH: 740
: TYPE: PRN
: ORGANISM: Acidothermus cellulolyticus
: US-10-155-400-6

```

Query Match	12.4%;	Score 130.1;	DB 9;	Length 740;
Best Local Similarity	10.6%;	Pred. No. 2.7e+02;		
Matches 70;	Conservative 31;	Mismatches 68;	Indels 489;	Caps 21.

QY	2	TIOP-----GTCYNNGYEYSV-----	-----MN	19
Db	2	TIOPYTWSNVVALGCGGFVDGIVFNEGAPCII	LYVRTIDIGMTAMDANCRMTPLLDWGMN	61
QY	20	D-GHGGVT-----	-----YTN-	29
Db	62	NMGYNVNSIAADPIINTKVMVAAGMYTNSMD	PNDGAILRSSDGGATWQITPLPFKLGGN	121
QY	30	-----GGCGGQPSVN-----	-----WNSGQNFV-----	46
Db	122	MGRGEMGERLAVDPPNDNLIYFGAPSGKGLMR	STDSGATWQMTNFPDVCYTIANPTDTT	181
QY	47	-----	-----GKQWQ--PCTKKKVI	60
Db	182	GYQSDIQGVVWAFDKSSSSLGQASKTIFVGV	ADPNNPVFWSRGGATWQAVPCAPGFI	241
QY	61	NFGGSINP-----	-----NCNSYLSVY	77
Db	242	PHKGVEDPVNHLYIATSNITGPRYDGSQDWK	FSVTSGTTRISPVPSPTDANDYFCGS	301
QY	78	G-----	-----MSR-----	81
Db	302	GLTIDRQHNTIMVATQISMWPDITIFRSTDG	ATWITIMDMTSYPNRSLRYULDISAEP	361
QY	82	-----NP-----	-----	83
Db	362	WTFGVQPNRPVPSPKLGWMDAMAIDFPNSDR	MLYGTGATLATNDLTKWDSGQIINIA	421
QY	84	-----	-----	87
Db	422	PWKGLEETAVNDLISPPSGAPLISALCDDG	FTHADYAVPSTIFTSPPVFTGTSTYDVA	481
QY	88	-----YIVENNGYVNPST-----	-----GATKLEGV-TSIDCS-----	113
Db	482	ELNPSILIVAGCSFDPSSQPNDRHNAFSTDG	CKNNFQSGSEPGGVTGGGIVAAASDGSRFW	541
QY	114	-----VYDI-----	-----YRTQFVNQPSI-TGTAFFYQ-----	138
Db	542	APGDQOPVYVAVGFCNSMAASQGVPAANAQI	RSRDVNPKEFYALNCGTFVFRSTDCGVTFQ	601
QY	139	SVKRNIRSSGSVNTANHFANAOQGLTGLTD	MYQIVANEBG-----YFSSGMS	186
Db	602	PVAAGLPSSGAV-----	-----GVMEHAAPCKEGQMLIAASSGLYHSTNGCS	643

RESULT 50 748-1554
US-09-880-748-1554
Sequence 1554, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PE523

; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1554
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1554

Query Match 12.4%; Score 129.9; DB 9; Length 251;
Best Local Similarity 15.5%; Pred. No. 48;
Matches 38; Conservative 23; Mismatches 33; Indels 151; Gaps 9;

OY 3 TOPG----- 6
: |||
Db 12 VQPGRSRLSCAASEFTFSNYAMHWROAPGKCLEWVAVISYDGTYSYADSMKGRFTIS 71
OY 7 -----TGYNNGYFYSYWMDHGCGVTYTG--- 30
Db 72 RDNKSNLYLQMSLRAEDTAVYICARENYDSLGTGYN--YFDYWGOG--TLVTVSSGGGG 128
OY 31 -----PGQFSYVMSNSNGNEVGK--GMQ---PGTKNKVI 60
Db 129 SGGGGSGGGGSAQAVLTQPSDSCGTPGQRTISMSSGSGSNISNAYSMTQQLPCTASKLL 188
OY 61 NMSGSTNPNG-----NSYLSYVGWSRNPLEYI-----VENEGTYNPST 100
Db 189 IYSNNLRPSGVPDRFSGSKSATSAALAIISGLQSEDEADYCAAMDPTLNAEYVFG----- 242
OY 101 GATKL 105
Db 243 GGTKV 247

Search completed: July 1, 2003, 11:58:36
Job time : 56 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 11:47:35 ; Search time 41 Seconds

(without alignments)
445.501 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045
Sequence: 1 OTIOPGTGYNNGYFYSYWMD.....YQIVAVEGYSFGSASITVS 190Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.73:*

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	222	2 S39154	xylinase 1 - fungus
2	1045	100.0	223	2 S39883	endo-1,4-beta-xylo
3	1022	97.8	190	1 A44594	endo-1,4-beta-xylo
4	1005	96.2	190	1 A44585	endo-1,4-beta-xylo
5	996	95.3	190	1 A44593	endo-1,4-beta-xylo
6	767.8	73.5	241	2 S71473	endo-1,4-beta-xylo
7	705.9	67.6	219	2 S71472	endo-1,4-beta-xylo
8	702.5	67.2	232	2 JC7577	endo-1,4-beta-xylo
9	684.9	65.5	225	1 S57469	endo-1,4-beta-xylo
10	670.9	64.2	221	1 S57469	endo-1,4-beta-xylo
11	656.8	62.9	221	2 JC7307	endo-1,4-beta-xylo
12	614.9	58.8	227	2 S43919	endo-1,4-beta-xylo
13	597.4	57.2	333	1 JS0590	endo-1,4-beta-xylo
14	597.4	57.2	335	2 TS0601	endo-1,4-beta-xylo
15	577.5	55.3	644	1 I40712	endo-1,4-beta-xylo
16	568.3	54.4	197	1 A44587	endo-1,4-beta-xylo
17	540.9	51.8	661	1 S59633	endo-1,4-beta-xylo
18	536.3	51.3	241	2 T37005	endo-1,4-beta-xylo
19	533.2	51.0	241	2 JS0591	endo-1,4-beta-xylo
20	530.9	50.8	656	1 S59631	endo-1,4-beta-xylo
21	527.4	50.5	240	1 S47512	endo-1,4-beta-xylo
22	527.3	50.5	210	2 C83762	endo-1,4-beta-xylo
23	506.2	48.4	213	1 I40569	endo-1,4-beta-xylo
24	505.2	48.3	213	1 S01734	endo-1,4-beta-xylo
25	505.2	48.3	213	1 S48126	endo-1,4-beta-xylo
26	472.8	45.2	354	1 S51779	endo-1,4-beta-xylo
27	467.6	44.7	228	1 WMB5XP	endo-1,4-beta-xylo
28	458.7	43.9	261	1 S12745	endo-1,4-beta-xylo
29	448.8	42.9	511	1 JQ1935	endo-1,4-beta-xylo

30	446.9	42.8	229	2 S39155	xylinase 2 - fungus
31	440.4	42.1	209	2 JC4909	endo-1,4-beta-xylo
32	434	41.5	211	1 S48229	endo-1,4-beta-xylo
33	432	41.3	211	1 S49542	endo-1,4-beta-xylo
34	430.9	41.2	211	1 JC1198	endo-1,4-beta-xylo
35	410	39.2	954	1 S20907	endo-1,4-beta-xylo
36	402.8	38.5	789	1 S58235	endo-1,4-beta-xylo
37	392.5	37.6	802	2 A36910	xylinase, beta(1,3
38	386.2	37.0	781	2 S51592	XyN precursor - R
39	316.1	30.2	607	2 S49528	endoxylinase - run
40	316.1	30.2	607	2 S24754	endo-1,4-beta-xylo
41	299.3	28.6	608	2 B53295	xylinase (EC 3.2.1
42	280	26.8	50	2 A61149	endo-1,4-beta-xylo
43	255.5	24.4	266	1 S48865	endo-1,4-beta-xylo
44	172.8	16.5	1441	2 A86685	prophage pil prote
45	170.9	16.4	2817	2 B97033	uncharacterized pr

ALIGNMENTS

```
RESULT 1
S39154
xylinase 1 - fungus (Trichoderma reesei)
C:Species: Trichoderma reesei
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C:Accession: S39154
R:Roerstroem, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkainen, N.; Harkki, A.; K
Biotechnology 10, 1461-1465, 1992
A>Title: The two major xylinases from Trichoderma reesei: characterization of both en
A:Reference number: S39154
A:Accession: S39154
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <TOE>
A:Cross-references: EMBL:X69573; NID:q396563; PIDN:CAA49293.1; PID:q396564
C:Genetics:
A:Gene: xyl1
A:Introns: 90/2
C:Superfamily: endo-1,4-beta-xylinase; endo-1,4-beta-xylinase homology
F:44-222/Domain: endo-1,4-beta-xylinase homology <XTL>

Query Match          100.0%; Score 1045; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.7e-39;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIOPGTGYNNGYFYSYWMDCHGCVTYTNGCGGFSVMSNSGNFVGCKGMPGTRKVI 60
    |||||||
DB 33 OTIOPGTGYNNGYFYSYWMDCHGCVTYTNGCGGFSVMSNSGNFVGCKGMPGTRKVI 92
    |||||||
QY 61 NFSGSYNPNNGSYLSVYGWMSRNPPIEYIVENPGYVNPSTGATKLGVTSPGSVYDIYRT 120
    |||||||
DB 93 NFSGSYNPNNGSYLSVYGWMSRNPPIEYIVENPGYVNPSTGATKLGVTSPGSVYDIYRT 152
    |||||||
QY 121 QRVNOPSIIIGATFYQYVSVRRNRHSSGSVYTNHFNMAAQGLTGMDOIVAVEGYF 180
    |||||||
DB 153 QRVNOPSIIIGATFYQYVSVRRNRHSSGSVYTNHFNMAAQGLTGMDOIVAVEGYF 212
    |||||||
QY 181 SSGSASITVS 190
    |||||||
DB 213 SSGSASITVS 222

RESULT 2
S39883
endo-1,4-beta-xylinase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)
N:Alternate names: endoxylinase II
C:Species: Trichoderma reesei
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C:Accession: S39883; S39884
R:Sarelaainen, R.; Palomäki, M.; Fagerström, R.; Suominen, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A>Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxy
```

A:Reference number: S39883; MUID:94088442; PMID:8264524
A:Accession: S39883
A:Molecule type: DNA
A:Residues: 1-223 <SAA>
A:Cross-references: EMBL:S67387; NID:9455906; PIDN:AB29346.1; PID:9455907
A:Experimental source: strain QM6a
A:Accession: S39884
A:Molecule type: protein
A:Residues: 34-43;49-57;121-151;178-191 <SAF>
C:Genetics:
A:Gene: xln2
A:Introns: 91/2
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <PRO>
F:20-33/Domain: propeptide #status predicted <SIG>
F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
F:45-223/Domain: endo-1,4-beta-xylanase homology <XYL>
F:71,94/Binding site: carbohydrate (asn) (covalent) #status predicted
F:110,121/Binding site: substrate (Tyr) #status predicted
F:119,210/Active site: Glu #status predicted

Query Match 100.0%; Score 1045; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.8e-39;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OTTPTGTGNNNGFYFYWMNDHGCGVYTTNGPGGQFVSVMNSNGNPFYGGKGMOPGTNNKYI 60
|||||
Db 34 OTTPTGTGNNNGFYFYWMNDHGCGVYTTNGPGGQFVSVMNSNGNPFYGGKGMOPGTNNKYI 93
|||||
OY 61 NFGSYNPNNGNSYLSVYGMNRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
Db 94 NFGSYNPNNGNSYLSVYGMNRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 153
|||||
OY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
Db 154 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 213
|||||
OY 181 SSGSASITVS 190
|||||
Db 214 SSGSASITVS 223

RESULT 3

A44594
endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
N:Alternate names: xylanase IIA
C:Species: Trichoderma viride
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 07-Nov-1997
C:Accession: A44594
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A:Reference number: A44593
A:Accession: A44594
A:Molecule type: protein
A:Residues: 1-190 <YAG>
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F:17,88/Binding site: substrate (Tyr) #status predicted
F:86,177/Active site: Glu #status predicted

Query Match 97.8%; Score 1022; DB 1; Length 190;
Best Local Similarity 97.4%; Pred. No. 2.8e-38;
Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 OTTPTGTGNNNGFYFYWMNDHGCGVYTTNGPGGQFVSVMNSNGNPFYGGKGMOPGTNNKYI 60

Db 1 OTTPTGTGNNNGFYFYWMNDHGCGVYTTNGPGGQFVSVMNSNGNPFYGGKGMOPGTNNKYI 60
|||||
OY 61 NFGSYNPNNGNSYLSVYGMNRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
Db 61 NFGSYNPNNGNSYLSVYGMNRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
OY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
OY 181 SSGSASITVS 190
|||||
Db 181 SSGSASITVS 190

RESULT 4

A44595
endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma
N:Alternate names: xylanase IIB
C:Species: Trichoderma viride
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 13-Mar-1998
C:Accession: A44595
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593
A:Accession: A44595
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-190 <YAG>
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F:86,177/Active site: Glu #status predicted
F:126,127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted
F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 96.2%; Score 1005; DB 1; Length 190;
Best Local Similarity 95.8%; Pred. No. 1.6e-37;
Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 OTTPTGTGNNNGFYFYWMNDHGCGVYTTNGPGGQFVSVMNSNGNPFYGGKGMOPGTNNKYI 60
|||||
Db 1 OTTPTGTGNNNGFYFYWMNDHGCGVYTTNGPGGQFVSVMNSNGNPFYGGKGMOPGTNNKYI 60
|||||
OY 61 NFGSYNPNNGNSYLSVYGMNRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
Db 61 NFGSYNPNNGNSYLSVYGMNRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
|||||
OY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHNANAAQGLTLGTMDYQIVAVEGYF 180
|||||
OY 181 SSGSASITVS 190
|||||
Db 181 SSGSASITVS 190

RESULT 5

A44593
endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (str
N:Alternate names: xylanase
C:Species: Trichoderma harzianum
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
C:Accession: A44593
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593
A:Accession: A44593
A:Molecule type: protein

[illegible][illegible]

Db 211 YQSSGSANV 219

RESULT 28

S12745

endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Clostridium acetobutylicum

N:Alternate names: xylanase B

C:Species: Clostridium acetobutylicum

C:Date: 30-Sep-1993 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999

C:Accession: S12745

R:Zappe, H.; Jones, W.A.; Woods, D.R.

Nucleic Acids Res. 18, 2179, 1990

A:Title: Nucleotide sequence of a Clostridium acetobutylicum p262 xylanase gene (xynB).

A:Reference number: S12745; MUID:90245673; PMID:2336398

A:Accession: S12745

A:Molecule type: DNA

A:Residues: 1-261 <ZAP>

A:Cross-references: EMBL:M31726; NID:g144933; PIDN:AAA23287.1; PID:g144934

A:Experimental source: strain P262

C:Genetics:

A:Gene: xynB

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-261/Product: endo-1,4-beta-xylanase B #status predicted <MAT>

F:72-255/Domain: endo-1,4-beta-xylanase homology <XTL>

F:152-242/Active site: Glu #status predicted

Query Match

Best Local Similarity 43.9%; Score 458.7; DB 1; Length 261;

Matches 89; Conservative 27; Mismatches 60; Indels 13; Gaps 4;

OY 8 GYNNGYFYSYWNDGCGVTTNGPGGQFSVWMSNGNFVCGK-----WDGTRNK 58

Db 68 GNGGYDYELMKD-YGNTSMFLKNGCAFSCQMSIGNALFRKGFNDOTYKLG--NI 124

OY 59 VINEGSGYNPNQNSLYSYGMSRNPLIEYIYVENGTNPISGATKLEVTSDSGYDIY 118

Db 125 SVNTDCNQPYPYNSLYCYGWTSSPLVEYIYDSGMSRPPGTSK-GLITVDGGIYDIY 183

OY 119 RTQVNPQSIIGTATFYQYWSVRRNRSSGSVNTANHFNAQAQGLTIGTMDYQIYAVEG 178

Db 184 ETRINQDSIOGNTTFKQYWSVRKTRISGTTISVSKHFAWDSKMPLGKMHETAFNIEG 243

OY 179 YFSSGSASAI 187

Db 244 YQSSGKADV 252

RESULT 29

J01935

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Clostridium stercoararium

N:Alternate names: xylanase A

C:Species: Clostridium stercoararium

C:Date: 30-Sep-1993 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999

C:Accession: J01935; P00531

R:Sakka, K.; Kojima, Y.; Kondo, T.; Karita, S.I.; Ohmura, K.; Shimada, K.

Biochem. Biotechnol. Biochem. 57, 273-277, 1993

A:Title: Nucleotide sequence of the Clostridium stercoararium xyna gene encoding xylanase

A:Reference number: J01935; MUID:93214115; PMID:7763496

A:Accession: J01935

A:Molecule type: DNA

A:Residues: 1-511 <SAK>

A:Accession: P00531

A:Molecule type: protein

A:Residues: 31-40 <SA2>

A>Note: the authors translated the codon AAC for residue 415 as Gly

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: Clostridium endo-1,4-beta-xylanase A; Clostridium xylanase A repeat ho

C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-511/Product: endo-1,4-beta-xylanase A #status predicted <MAT>

F:44-228/Domain: endo-1,4-beta-xylanase homology <XTL>

F:237-368/Region: linker

F:273-368/Domain: Clostridium xylanase A repeat homology <CXA1>

F:413-506/Domain: Clostridium xylanase A repeat homology <CXA2>

F:124-215/Active site: Glu #status predicted

Query Match

Best Local Similarity 42.9%; Score 448.8; DB 1; Length 511;

Matches 90; Conservative 24; Mismatches 59; Indels 22; Gaps 5;

OY 7 TGINNGYFYSYWNDGCGVTTNGPGGQFSVWMSNGNFVCGKQPGTKK----- 58

Db 39 TGTGNGYDYELMKD-YGNTIMELNDGTFSCQMSIGNALFRKG-----RFNSDKTYQ 91

OY 59 -----VINEGSGYNPNQNSLYSYGMSRNPLIEYIYVENGTNPISGATKLEVTS-DG 112

Db 92 ELGDIVYEXGCDYNNNGNSLYCYGWTNPPLVEYIYVDSGMSRPPGATPKGTTQMA 150

OY 113 SVYDIYRTQVNPQSIIGTATFYQYWSVRRNRSSGSVNTANHFNAQAQGLTIGTMDYQ 172

Db 151 GTYEIVETTRVNPQSIDGATFYQYWSVRTSKRTSGTISVEHFQWRMGMRMGKMYEV 210

OY 173 IVAVGTFSSGSASI 187

Db 211 ALTEGQYQSSGVANY 225

RESULT 30

S39155

xylanase 2 - fungus (Trichoderma reesei)

C:Species: Trichoderma reesei

C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999

R:Toerrien, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkinen, N.; Harkki, A.; K

Biotechnology 10, 1461-1465, 1992

A:Title: The two major xylanases from trichoderma reesei: characterization of both en

A:Reference number: S39154

A:Accession: S39155

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-229 <TOR>

A:Cross-references: EMBL:X69574; NID:g396565; PIDN:CAA49294.1; PID:g396566

C:Genetics:

A:Gene: xyn2

A:Introns: 97/2

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

F:53-228/Domain: endo-1,4-beta-xylanase homology <XTL>

Query Match

Best Local Similarity 42.8%; Score 446.9; DB 2; Length 229;

Matches 98; Conservative 22; Mismatches 50; Indels 21; Gaps 6;

OY 1 OTIQPGTGYNNNGYFYSYWNDGCGVTTNGPGGQFSVWMSNGNFVCGKQPGTKKVI 60

Db 58 QNYQYG-----GOVSYSPSNTG-FSVWMTQDDFVVGWTTGS-SAPI 99

OY 61 NFSGSGYNPNQNSLYSYGMSRNPLIEYIYVENGTNPISGATKLEVTSDSGYDIYR 119

Db 100 NFGSGFSVNSGTLGLSVGWSNPLVEYIYEDNINY-PAQGYTK-GLVTSQDGAITYTWE 157

OY 120 TORVNPQSIIGTATFYQYWSVRRNRSSGSVNTANHFNAQAQGLTIGTMDYQIYAVEGY 179

Db 158 NTRVNEPSIQGTATFQYISVNSPRTSGTIVQHHFNAMASLGHLCQMMYQVAVYEGW 217

OY 180 FSSGSASITVS 190

Db 218 GSGSASQSVS 228


```

OY 64 GSYPNMNG-SYLSYVSGSRNPLLEYIVENGTNPSHGATKLEGVSDSGVYDIKTR 122
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 AEYSASGASTLAYGWMNPDAEYIVEDYEDGNPCSSASLCTIVSDGSTVOYCTDTR 142
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 123 VNPSIIIGTATFYQWYSVRNRHSSGSVYNTAHNFNAMAQOGLTGTMDYQIVAAEGYFSS 182
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 TNEPSITGTSFTFYQYFSVRESTRFTSGTYVANHHNFMAHHFGNSDFNYQVVAEAMSGA 202
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 183 GSASITVS 190
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 GSASVTVIS 210

RESULT 34
JC1198
endo-1,4-beta-xylanase (EC 3.2.1.8) C precursor - Aspergillus niger
N:Alternate names: xylanase C
C:Species: Aspergillus niger
C:Date: 05-Mar-1993 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
C:Accession: Jc1198; PS0436
R:Ito, K.; Iwashita, K.; Iwano, K.
B:BioSci. Biotechnol. Biochem. 56, 1338-1340, 1992
A:Title: Cloning and sequencing of the xync gene encoding acid xylanase of Aspergillus
A:Reference number: Jc1198; MUID:93005082; PMID:1368843
A:Accession: Jc1198
A:Molecule type: DNA
A:Residues: 1211 <IT0>
A:Accession: PS0436
A:Molecule type: protein
A:Residues: 28-34 <IT01>
A:Note: the source is designated as Aspergillus kawachii
C:Genetics:
A:Gene: xync
A:Introns: 77/72
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase: endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-211/Product: endo-1,4-beta-xylanase C #status experimental <MAT>
F:30-210/Domain: endo-1,4-beta-xylanase homology <XYL>
F:106,197/Active site: Glu #status predicted

Query Match 41.2% Score 430.9; DB 1; Length 211;
Best Local Similarity 44.0%; Pred. No. 3,1e-12;
Matches 88; Conservative 28; Mismatches 53; Indels 31; Gaps 6;

OY 21 GH-----GGVYTT---NG-----PGQFVSVMNS--SGNFVGKGM 51
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 12 GHAFAPAPQPVVLYSRSGINQVQNYNGNLADPTFDEAGTFSMWEKGVSDPYVGLGW 71
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 52 QPGRKNKYINFGSINPNG-NSYLSVYGWSRNPLEYIVENFGTNPSTGATKLEGVTS 110
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 TTGSN--AISYSAEYSASGSSSYLAIVGWMVYPOAEYIVEDYDGNPCSSATSLGTVYS 130
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 111 DGSVYDIIRQORVNOPSLIGTATFYQWYSVRNRHSSGSVYNTAHNFNAMAQOGLTGM 170
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 DGSYVQCTDTRTREPSTLTGTFTFYFSVRESTRFTSGTYVANHFMAHFGNSDFN 190
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 171 YQIVAVEGEFSSGSASITVS 190
    1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 YQVMAVEAMSGAGSASVTVIS 210

RESULT 35
S20907
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor, bifunctional - Ruminococcus flavefaciens
N:Contains: endo-1,4-beta-xylanase (EC 3.2.1.8)
C:Species: Ruminococcus flavefaciens
C:Date: 22-Nov-1993 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999
C:Accession: S20907; S18043

```

R: Zhang, J. X., Flint, H. J.
Mol. Microbiol. 6, 1013-1023, 1992
A: Title: A bifunctional xylanase encoded by the xyna gene of the rumen cellulolytic bacterium
A: Reference number: S20907; MUID:92261318; PMID:1584021
A: Accession: S20907
A: Molecule type: DNA
A: Residues: 1-954 <2NH>
A: Cross-references: EMBL:Z11127; NID:946161; PIDN:CAA77476.1; PID:9581505
A: Experimental source: strain 17
C: Genes: xyna
A: Gene: xyna
A: Start codon: TTG
C: Function:
A: Pathway: xylan degradation
A: Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
C: Superfamily: Ruminooccus bifunctional endo-1,4-beta-xylanase; endo-1,4-beta-xylanase
C: Keywords: extracellular protein; glycosidase; hydrolase; multifunctional enzyme; po
F: 1-37/Domain: signal sequence #status predicted <SIG>
F: 28-954/Product: bifunctional endo-1,4-beta-xylanase #status predicted <NMT>
F: 28-248/Domain: catalytic domain A #status predicted <CDA>
F: 40-236/Domain: endo-1,4-beta-xylanase homology <XYL>
F: 249-652/Domain: linker region B #status predicted <LRB>
F: 652-954/Domain: catalytic domain C #status predicted <CCC>
F: 653-953/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>
F: 122, 223/Active site: Glu #status predicted

	Query Match	39.2%	Score 410:	DB 1:	Length 954:
	Best Local Similarity	41.4%	Pred.	5.2e-10:	
	Matches	84:	Conservative	33:	Mismatches 66: Indels 20: Gaps 6
Oy	4 QPQGTGNNGYFYSYNDHGAGVTTYTNGPGQGSFYVMSSNSGNFEVG--GKGMPGTKNK---	58			
Db	32 QQRGVNNGVDYEDMNMNQNGOASNMHPGAGSPFCSSNIENFLARMKNGYDSOKKNYKAF	91			
Oy	59 ---VINFGSYNNGSNGLSYLVYGMSRNPLLEYIYIENGCTNP--SGATKRLGEVTSDGS	113			
Db	92 GNIVLTVYDEYTPRGNSICYGVGMTRNPLMEYYIEVGGDWPRPNODEYA-GTVSANGN	150			
Oy	114 VYDIYFTORYNQPSLIIGTAIFYQYSVRNRHRS-----GSYNTANHHNAQAQGLT	165			
Db	151 TYDIRKTMRYNQPSLDGGTATPPQYVSVRQTSSANNQNTNYMKGITDYKHFDAMSAAGLD	210			
Oy	166 LGTMDYQI-VAAEGYSSGSASI	187			
Db	211 MSGTLVEYSLNTEGRYSNSAVV	233			

RESULT 36
S58235
endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - Ruminococcus sp.
N:Alternate names: xylanase 1
C:Species: Ruminococcus sp.
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jun-2000
C:Accession: S58235
R:Atakali, C.; Brives, R.; Czihal, A.; Beaumlein, H.; Carillo, B.; Hofemeister, J.
Submitted to the EMBL Data Library, June 1995
A:Description: Xylanase 1 from Ruminococcus sp. with a new pattern of domain shuffling
A:Reference number: S58235
A:Accession: S58235
A:Molecule type: DNA
A:Residues: 1-189 <ARA>
A:Cross-references: EMBL:Z49970; NID:g929842; PIDN:CAA90271.1; PID:g929843
C:Genetics:
A:Gene: xynI
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylonic acid bonds in xyans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase homology: Thermotoga xylanase A amino-terminal
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-789/Product: endo-1,4-beta-xylanase #status predicted <MAT>


```
RESULT 40
S24754
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - rumen fungus (Neocallimastix patriciarum)
N:Alternate names: xylanase A
C:Species: Neocallimastix patriciarum
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Oct-1999
C:Accession: S24754; S21392
R:Gillbert, H.J.; Hazlewood, G.P.; Laurie, J.I.; Orpin, C.G.; Xue, G.P.
Mol. Microbiol. 6, 2065-2072, 1992
A:Title: Homologous catalytic domains in a rumen fungal xylanase: evidence for gene dupl
A:Reference number: S24754; MUID:93023832; PMID:1406248
A:Accession: S24754
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-607 <GIL>
A:Cross-references: EMBL:X65526
R:Gillbert, H.J.; Hazlewood, G.P.; Laurie, J.I.; Orpin, C.G.; Xue, G.P.
submitted to the EMBL Data Library, April 1992
A:Description: Homologous catalytic domains in a rumen fungal xylanase: evidence for gen
A:Reference number: S21392
A:Accession: S21392
A:Molecule type: mRNA
A:Residues: 1-152, 'S', 154-607 <GIL>
A:Cross-references: EMBL:X65526; MID:93090; PIDN:CAA46498.1; PID:93091
C:Genetics:
A:Gene: xyna
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-607/Product: endo-1,4-beta-xylanase #status predicted <MAT>
F:46-242/Domain: endo-1,4-beta-xylanase homology <XYL1>
F:291-487/Domain: endo-1,4-beta-xylanase homology <XYL2>

Query Match          30.2%; Score 316.1; DB 2; Length 607;
Best Local Similarity 34.0%; Pred. No. 2.8e-06;
Matches 69; Conservative 38; Mismatches 72; Indels 24; Gaps 6;

QY 8 GYNNCFYSYNNNDGHC-G-VTTNPGGQPSVWMS---NSGNFVGKGMQPGTKNV---- 59
DB 287 GYNNDFSYEIMLDNMGSGMTLGSATFKAEMNAAVNRGNFLARGLDFGSGKATDYD 346
QY 60 ---INFSQSY---NPNNSYLSYSGMSRN-----PLEXYIVNFCGYNPSGTATRLG 106
DB 347 YIGLDYAAATYKOTASASGNSRLCYTGMFONGLNGVPLVEYIIIDWDWDPDAOGKM-- 404
QY 107 EVTSDGSYYDIYRTQRVNQPSTIGTATFYQYWSVRNRHSSGVSNTANHFNMAAOGLTL 166
DB 405 -VTIDGAGYKIFQMDHTGPTINGSETFKQYFSVRQKRTSHILVDSHFKEKMAQNGMI 463
QY 167 GTMDYQIYAVEGYFSSGSASITV 189
DB 464 GNLVEVALNAEGWSSGVADYTL 486

RESULT 41
BS3295
xylanase (EC 3.2.1.-) precursor - Fibrobacter succinogenes
N:Alternate names: xylanase 2
C:Species: Fibrobacter succinogenes
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 08-Oct-1999
C:Accession: BS3295
R:Paradis, F.W.; Zhu, H.; Krell, P.J.; Phillips, J.P.; Forberg, C.W.
J. Bacteriol. 175, 7666-7672, 1993
A:Title: The xynC gene from Fibrobacter succinogenes S85 codes for a xylanase with two s
A:Reference number: A53295; MUID:94064561; PMID:8244936
A:Accession: BS3295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-608 <PAR>
A:Cross-references: GB:U01037; MID:9402870; PIDN:AAA21848.1; PID:9402871
```

```
C:Genetics:
A:Gene: xynC
C:Superfamily: endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase
F:51-250/Domain: endo-1,4-beta-xylanase homology <XYL1>
F:327-514/Domain: endo-1,4-beta-xylanase homology <XYL2>

Query Match          28.6%; Score 299.3; DB 2; Length 608;
Best Local Similarity 33.0%; Pred. No. 1.5e-05;
Matches 69; Conservative 32; Mismatches 71; Indels 37; Gaps 7;

QY 8 GYNNC-----YFYSYNNNDGHCYVYTNNGPGQPSVWMSNGNFVGKGMQPGTKN 57
DB 313 GONNSYVTGNVSSPYHVEIHWQC-GNNSMTFYDNGTYKASWNGTNDFLARGEKXDEKH 371
QY 58 KVINP-----SGSYNNGNSYLSYVQMSNPLEXYIVNFCGYNPSGTAT 103
DB 372 TYEELGPIDAYYKWSKQSGAGYN---YIGYGVTDVPLVEYIYVDW--FN-KPGAN 423
QY 104 KL---GEVTSYDGSYYDIYRTQRVNQPSTIGTATFYQYWSVRNRHSSGVSNTANHFNAW 159
DB 424 LLGQRKGEFTYDGDYELTWMTRVQGPSIKGTQFPQYFSVRKASRSGCHIDITAHMKKM 483
QY 160 AQQGLTCTMDYQIYAVEGYFSSGSASITV 188
DB 484 EELGKMKGMKMYEAKVLEAGSGSGSFVDT 512

RESULT 42
A61149
endo-1,4-beta-xylanase (EC 3.2.1.8) - fungus (Trichoderma viride) (fragment)
C:Species: Trichoderma viride
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 31-Jan-1997
C:Accession: A61149
R:Ujite, M.; Roy, C.; Yaguchi, M.
Appl. Environ. Microbiol. 57, 1860-1862, 1991
A:Title: Low-molecular-weight xylanase from Trichoderma viride.
A:Reference number: A61149; MUID:91336731; PMID:1872616
A:Accession: A61149
A:Molecule type: protein
A:Residues: 1-50 <UJI>
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation; pyroglyutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match          26.8%; Score 280; DB 2; Length 50;
Best Local Similarity 94.0%; Pred. No. 7.6e-07;
Matches 47; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGCTYNNGYFYSYNNNDGHCYVYTNNGPGQPSVWMSNSGNFVGKG 50
DB 1 OSIGGTGFNNGYFYSYNNNDGHCYVYTNNGPGQPSVWMSNSGNFVGKG 50

RESULT 43
S48865
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - rumen fungus (Neocallimastix fronta)
N:Alternate names: xylanase 2
C:Species: Neocallimastix frontalis
C:Date: 13-Jan-1995 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999
C:Accession: S48865
R:Durand, R.; Fevre, M.
submitted to the EMBL Data Library, November 1994
A:Description: The xyn2 gene of the anaerobic fungus Neocallimastix frontalis.
A:Reference number: S48865
A:Accession: S48865
A:Molecule type: mRNA
A:Residues: 1-266 <DUR>
A:Cross-references: EMBL:X82439; MID:9565625; PIDN:CA57820.1; PID:9565626
C:Genetics:
```

A:Gene: XYN2
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-54/Domain: signal sequence #status predicted <SIG>
F:55-266/Product: endo-1,4-beta-xylanase 2 #status predicted <MAT>
F:67-266/Domain: endo-1,4-beta-xylanase homology <XYL>
F:150,243/Active site: Glu #status predicted

Query Match	24.48;	Score 255.5;	DB 1;	Length 266;
Best local Similarity	28.68;	Pred. No. 0.00025;		
Matches 59;	Conservative 35;	Mismatches 67;	Indels 45;	Gaps 8

```

QY      11  NGVFPYSYND--GHGCVATYNGGCGGFVSMXMSNGNVGGRKQPGTKNKYINFGS-----65
Db      66  NGIGELMADSDNNNSATFYD--DGSFSCGFOAKDYLCNSG-----LSFDSTRKTHK 114

QY      66  -----YMPNGNSLYLVXGWSHNPILLEYIVENF--GYNPS--TGA 102
Db      115 QIGHIYAEPKLYKQNIQNDY-----SYVGIVGWTRNPLVEFYVDNMILSOMRPGDWYGN 169

QY      103 TKLGEVTSDEGSYYDIYRTQVRVNOPSTIGTATFYQIWSVVRNRHRSQSVANTANHFMAAQO 162
Db      170 KKHGFTTIDGAQYTYENTRYG--PSIDGDTFNKQFYRSIROOPRDCCTIDITAHFEOMEKL 228

QY      163 GLLGTMDYQIYAVEGFSSGSAST 188
Db      229 GMTGCKMHEAKVLGEGSNNGTSGT 254

```

RESULT 44
A86685

C:Species: *Lactococcus lactis* subsp. *lactis*
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: AB6685
R:Botolin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s
A:Reference number: AB6625; MUID:21235186; PMID:11337471
A:Accession: AB6685
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1441 <SPRO>
A:Cross-references: GB:AA005176; PID:g12723361; PIDN:AAK04579.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: p1146

Query Match	16.5%;	Score 172.8;	DB 2;	Length 1441;
Best Local Similarity	10.4%;	Pred. NO. 31;		
Matches	84;	Conservative	34;	Mismatches 67;
				Indels 622;
				Gaps 23

Oy	2	TIOPGTGNN	----	GYFYSV	----	WNGCHGG	-----	24
		: :				: :		
Db	608	TVTPTGTGTSQVPLVKEOYLMTKTLMTYTDNTSEGGYSVSI	AKGNGNHGDFGKGDV	667				
Oy	25	-----						24
Db	668	GISMTIEYGVAGSCTSKPTGCMSTTPTVPAGOLMTPTTQYTDGTS	EOGINALMGI	727				
Oy	25	-----						36
		-VTY- -TNG- -PGQFS-						
Db	728	TGASGRDGIAGDKGIGKATATITYOASTNGTAPGTMTSTVSPVAKGS	SFLMTRTIIMYT	787				
Oy	37	-----	-VWMSNGSFGVCGK			-GMQ-		52
		: :						
Db	788	DNTTETGYAVAVMGNGNNGTNGIAGKDDTGIKTTTITVAVGTS	GTTAPGKMN	847				
Oy	53	-----				-PCTK-		56

Dd	848	PAGCVLWMTKTYDWDYDTRKTSFSGYSVKRKGKEDKDDQGVQIGQVADGRGIGRPGADCK	907
QY	57	-----NKVYINFGS-----YVPCNGNSYLSYVGWS-----	80
Dd	908	TQYTHIAVANSADGKTNEFSTDSNRRTYIGMYVDENINSDTPSPDYSWTLVKGADGTQCTP	967
QY	81	-----NPNLEIYI-----VENPGYINPS-----TGATK-----	104
Dd	968	GKPGTGDGTP--FYHTAMYSYADGTDGFTTYVYPMILNLLDGTSKSAKTATYIKDDVAGII	1022
QY	105	-----LEKVTSDGSSVY-----DIYRTQV-----	123
Dd	1025	YMDTRKQJSEKTIITGSVYLDLTNPSYDVAWFQOLYTTNGVLXGNTIKAGQKGYRFSFGKSVTI	108
QY	124	-----NOPSIIIGATEYQ	136
Dd	1085	TDNNANIAFRTPTKVDTITFDYSEMKIEEGSTATPYMPSKKTADYAPSYIGQYTDPK	114
QY	137	Y-----WS-----	139
Dd	1145	QSDSTNPSDYTWMSLIRGNDGDPGKVVSDTEPTTRFKGLTWKYSTADLTASDGTYIKPNT	120
QY	140	-----VRRNH	144
Dd	1205	EYYINGTHTWMINYUSANNIEANSIKADKIDAKNLTITDGEFVSTTNGPVTYSTEIKDNH	126
QY	145	-----RSSGSVYTAHFNFAMAOOG-----	163
Dd	1265	IAISTDGTVTMKNDLAVDTBEGFAMKFTTNNTTGLTREASVNFQGVSTSDSGNVAQLTLP	132
QY	164	-----LTJGTYNDY	171
Dd	1325	QGTKLSTDPWTDILTRASGVGTGTLARLRINNGVEYAOOSKDVITPISIAPNSLITIGTWS	138
QY	172	QIVAAEYQ-----FSSGS-----ASTTV	189
Dd	1385	KFSGVSGFDTLGLLYSPQGLSVASATV	1411

RESULT 45
B97033
uncharacterized protein, related to enterotoxins of other Clostridiales [Imported] -
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_text15ion 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: B97033
R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; I
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97033
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-2817 <R>
A:Cross-references: GB:AE001437; PUDN:AAK79053.1; PUD:G15023993; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1079

Query Match	16.48;	Score 170.9;	DB 2;	Length 2817;
Best Local Similarity	11.68;	Pred. No. 1.4e+02;		
Matches 80;	Conservative 35;	Mismatches 63;	Indels 511;	Gaps 24

OY	I OTIQPGICYNNGY-----FYSIWN-----DGH--GGVYTITG--	--30
Dd	1134 QTIIR---YNNRGYSSEFYNTYYFNSDGTAKTGFETYLANKTYFFNPSDGRLMOYOXINGH	1189
OY	31 ---PCGOFSVMNSNCN-----FVG--+	47
Dd	1190 YTFAPDMGMQWGITNSSKYYLDPSGAAYTGLOTINGNKRYCFDSNGILQHNGIFRICHT	1246
OY	48 -----GK-----	49

Db 1250 YKSDNNGIMLTGLDLINGLYLCFNSDSGSKTGLVLTGKTYYPDSYSVSGFQINNNNTY 1309
QY 50 -----GMP-----GTRKVINSGSY-- 66
Db 1310 YFGNDGTMTGWNVNGYRYRYLNDGSIKATGMQTTIDGKNKYFDYGAKTGIVNIDGNTYG 1369
QY 67 -----NPNNGSY- 73
Db 1370 FNNSGVMLTGMQHNGSTYFNSNGIANTGFTLYLGTYYFPDSYGRMOTISMTINTSTY 1429
QY 74 -----LSYFGMSRNPLEYIIVENFT----- 95
Db 1430 FYANGVMKTSTDSPTMLAV-GWVRDSYXYQYYLMAAGTKLTGLQIDGNTYFDSNGIMQ 1488
QY 96 -----YNPSGATKLEGVSDGSYV--DIYROR 122
Db 1489 TGLITINGNRGYFGVNGWLYGLQFINNNFTYNSYISGTFPVLGNTYFDSIGEMR 1548
QY 123 V-----NPSI----- 128
Db 1549 IGLTYINNNYFNSGIMETGMISLYRYANPNGLITGFTINCKTYFNSDGLLYL 1608
QY 129 -----IGATFY-----OYWSYRNH 144
Db 1609 QYNGSYGFDKNGWLYGLQITIGNTYLNNGISQSGFTLNGKTYFDSYGMRTGI 1668
QY 145 RS-----SGSVNT-----AN-----HFNMAQ----- 161
Db 1669 QVINNNYFFGNGTLQGTWISODNLRYANSSGCLTGLQTTIDGKKYFNSYARETGL 1728
QY 162 -----OG----- 163
Db 1729 VYINNTYGFNDGTLTYSWNNHNGRMVCFNTDGTVKTWIMVLGKSCVLDSSQGLSLNG 1788
QY 164 -LTLG-----TMDQIYAVEGFSSGSA 185
Db 1789 LTTIGNIYFSGDYSMT--GWTSGSS 1815

RESULT 46

S76412
hypothetical protein slr0408 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #extl_change 20-Jun-2000
C:Accession: S76412
R:Kaneko, T.; Sato, S.; Kottani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76412
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4199 <KAN>
A:Cross-references: EMBL:D90915; GB:AB001339; NID:q1653604; PIDN:BA018541.1; PID:q165362
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: *Synechocystis* hypothetical protein slr0408

Query Match 15.9%; Score 166.3; DB 2; Length 4199;
Best Local Similarity 10.8%; Pred. No. 5e+02;
Matches 78; Conservative 29; Mismatches 65; Indels 547; Gaps 19;
QY 1 QTIOPG-----TGYNNGYFYSWNDGHGVYTTNGPG 32
Db 3010 QTIOMGGDQANQVWTVNATNWNSSRPFAVLIGOSNGDIWY-----PG 3056
QY 33 G-----QFSVNSNSGN-----FVGKSG----- 50
Db 3057 GNNOMSGCKLPALNELAVNMNTSGNPOTIAGLGKGIIEYNGSTWVNGPQGDGMR 3116
QY 51 -----WQPGTKN 57

Db 3117 SAITQAMAVQMGEDGSPSLQVLGLADGAVIYNTQSGMRTINNFGKSVTQLSVQMOEASNP 3176
QY 58 KVI----- 60
Db 3177 NIVGLDNSEVOYQYQSGNCGWTFQPHDDGKVVYEVQOLAVQWTSNDAPLVVGLGDGNGN 3236
QY 61 -----NFGSGYNPNGN----- 71
Db 3237 GSWYTYQSGEGGQWTFSLGLPSGAALQAMAVQWNFSSPFPNNVNDLKIYVGQADSYV 3296
QY 72 SYLSYVQMSRNPDI-----EY----- 87
Db 3297 SYTNGNGWATPAINSLIQITLNAITVQWSANGQPQITVGLGDEYDNGQLWYLPNPQ 3356
QY 88 -----YIVENFTYNS-----TGA-----TKL 105
Db 3357 SMOELQSVNVASPIQTQIDSSWTSLSLVPNSQTDNLVYFEGSDPNDYVNTGTIGDDVAV 3416
QY 106 GEVTSQD-----GSYDIYRQ----- 121
Db 3417 GSATGESFLAGGDDQILTKGLDVVYAGPGDWVSVSDTYRRLNGTGFDILALQYN 3476
QY 122 -----RVNPSIIGTAT----- 133
Db 3477 GGNMDLTLSPLRLQDFETIDIRQGANQLTLNLSLVSNNMTYIVLMDSGDSLQ 3536
QY 134 -----FYQWS----- 139
Db 3537 SSDFGADGTTYQYQGRFYQYKSSNNSAIVLVNQPTMPSPFTAPSONKPOPVLNCGTSM 3596
QY 140 --VRRNHRSSGSVNTAN-----HFNMAQOGLT----- 165
Db 3597 AALNTNIAANTGANNGNFENDENINTGNANTGNFN-----NGNTNTGNGVDINIAATLFPSS 3652
QY 166 -----LGTMDYQI-----VAVEGYFSSGSASITV 189
Db 3653 PTASEALGEVDFTIERTGDLDRKYVVSYLQDMDGACGRILYPVAGQLFKRGEIKRTI 3711

RESULT 47

A42296
lysozyme 2 (EC 3.2.1.-) precursor - *Enterococcus hirae* (ATCC 9790)
C:Species: *Enterococcus hirae*
C:Date: 10-Jul-1992 #sequence_revision 18-Sep-1992 #extl_change 15-Oct-1999
C:Accession: A42296
R:Chu, C.P.; Kariyama, R.; Daneo-Moore, L.; Shockman, G.D.
J. Bacteriol. 174, 1619-1625, 1992
A:Title: Cloning and sequence analysis of the muramidase-2 gene from *Enterococcus hirae*
A:Reference number: A42296; MUID:92165737; PMID:1347040
A:Accession: A42296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-666 <CHU>
A:Cross-references: GB:M7639; NID:q148303; PIDN:AA424776.1; PID:q148304
A:Note: the authors translated the codon GGT for residue 171 as Tyr
C:Keywords: glycosidase; hydrolase

Query Match 15.7%; Score 163.6; DB 2; Length 666;
Best Local Similarity 17.5%; Pred. No. 17;
Matches 70; Conservative 28; Mismatches 68; Indels 234; Gaps 16;
QY 7 TGYNNGYFY-SYW-----N 19
Db 161 TSGMGYYVYAGTWKSNTKSYDTACLTGRYATDPQYACKLNNITTYGLTRYDTPASGN 220
QY 20 DGHGCVTYTNGPG-GQFSVNSNSGNFVGGKMQPCT----- 55
Db 221 AG-GCVTTCGNTGNTGNTSGNSTGN-SGGSATTTGTTTYVSGDSYMGISHPGTTMAQ 278
QY 56 -----KNKVI-----NFGSYNPNNGNS----- 72
Db 279 LIEWNINKNFYPCQKLTIKGGQSGSSTTNTGNNASSGNTSGNTNTSGSTGQATGAKY 338

```

OY 73 -----YLSYGWSRNPLIEYIYENGT-----NSTCAT 103
DB 339 TVKSDSWKTIANDIGISMNOLIEMNNIKNNFYPGQOLVWSKSSSASGSTSNTSTGT 398
OY 104 -----KLGEDVSDGSVDYIFRTORVNPISIIGTATFYOWWSYR----- 142
DB 399 SSNTANTOSTTS-GSTYTVKAGESEY-----WSSNKFISMNOLIOMNNK 443
OY 143 -----NHSSGVSNTANHFN-----AMA---Q 161
DB 444 NNEIYPGOKLIYKGGSSSSNASTSPANKNNPAASSNTSSTATGOATYTVKAGESEWGVANK 503
OY 162 OGLTIGTM-----DYQIYAEGYFSSGSASTIV 189
DB 504 NGISMNOLIEMNNIKNNFYPGOKLIYKGGSSKASATATI 543

RESULT 48
D70575
Probable_PPE_protein - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: D70575
R:COLE, S.T.; BRODSCH, R.; PARKHILL, J.; GARNIER, T.; CHURCHER, C.; HARRIS, D.; GORDON, J.; CONNOR, R.; DAVIES, R.; DEVLIN, K.; FELLWELL, T.; GENTILE, S.; HAMLIN, N.; HOLROYD, S.; RAJANDREAM, M.A.; ROGERS, J.; RUTTER, S.; SEEGER, K.; SKELTON, S.; SQUARES, S.
Nucleotide 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:96295987; PMID:9634230
A:Accession: D70575
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-3300 <COL>
A:Cross-references: GB:295324; GB:AL123456; MID:93261760; PIDN:CAB08587.1; PID:e1299834
A:Experimental source: strain H37Rv
A:Genetics:
A:Gene: PPE

Query Match 15.7% Score 163.6: DB 2: Length 3300;
Best Local Similarity 12.4% Pred. No. 4e+02;
Matches 65: Conservative 37; Mismatches 57; Indels 364; Gaps 18;

OY 2 TIOPGTGYNN-----GYF-----YSYWN-- 20
DB 1844 TTPPSGFNFNMGTGTGVSGVNGVSSGFFNLTSSSSGISGVQNRGELISGFFNFGTYS 1903
OY 21 ----- 20
DB 1904 GLVNASTLGLSMPANLSCGVAVGATVAGFVNNTQILNLFENVSGVNGHGNIGDSNVGL 1963
OY 21 -----GHGGV-----TYTNGP-----GQFSSNW 39
DB 1964 GNLCNANVGHGNIGSFNVFSCGNRGSYNTGPANLGNYNIGLCNLGSYNFPGNAGDFNLF 2023
OY 40 SNSGN-----FYVGKG-- 50
DB 2024 ANSGSNNGFANTGNNNIGIGLSCHNQGFCSMSNGTANTGLFNSTGNTNIGLFGNIGTNI 2083
OY 51 -----WPGTKNKVYNFSGSYNPG-----NS 72
DB 2084 GIGNSGIGNTGIGNPGVNTGLGNSGTGMCLMNPCTNMKVAVNGTYNTGYNVWGTYNT 2143
OY 73 YLSYGWSRNPLIEYIYENGTYNPSGATKRLGEVTSDSGV-----YD-IYPTQ 121
DB 2144 GIANYG-----IANTGSTN--TGSTNTGSF--NDGPNTEGYNTGDTNTEGYNTG 2189
OY 122 RVNPSIIGTATFYOWWSVRRNHRSSGSVANTANHFNNAN-AAOGLTL----- 166
DB 2190 DVNTGAGTGC-----GNFSNGAFMGSDHQGCGAHATYATVQIPIPLNLSLNPV 2237
OY 167 -----GTN---DYQIYAV----- 176

```

Db 2238 NIPHLDFGLTAVNGFQIPLATLALGVTHESVGPILVRACGLPVIDINIGDPGSSS 2297

OY 177 -----EGYRSSGSAS 186
 |::||:|

Db 2298 IPITTSAGCPVPIPLDIPAPGFGNSTGTSPSSGFNPGSGS 2340

RESULT 49

JF00001
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Rhizopus oryzae
N:Alternate names: 1,4-alpha-D-glucan glucohydrolase; glucoamylase
C:Species: Rhizopus oryzae
C:Date: 28-Dec-1987 #sequence_revision 23-Aug-1996 #text_change 16-Jun-2000
C:Accession: JF00001

R:Ashikari, T.; Nakamura, N.; Tanaka, Y.; Kluech, N.; Shibano, Y.; Tanaka, T.; Amachi,
Agric. Biol. Chem. 50, 957-964, 1986
A>Title: Rhizopus raw-starch-degrading glucoamylase: its cloning and expression in ye
A:Reference number: A90022
A:Accession: JP00001

A:Molecule type: DNA
A:Residues: 1-604 <ASH>
A:Cross-references: GB:D00049; PIDN:BAA00033.1; PID:g218035
A:Experimental source: strain SAM0034
A>Note: there are two errors in the published sequence (personal communication): GCT
Y to the known amino acid sequence of 11 peptides from glucoamylase, including the am
R:Tanaka, Y.; Ashikari, T.; Nakamura, N.; Kluech, N.; Shibano, Y.; Amechl, T.; Yoshiz
Agric. Biol. Chem. 50, 965-969, 1980
A>Title: Comparison of amino acid sequences of three glucoamylases and their structur
A:Reference number: A90023
A:Contents: annotation; homology; predicted secondary structure
C:Comment: Rhizopus glucoamylase exists in multiple forms, Gluc 1, Gluc 2, and Gluc 3
and degrade raw starch.
C:Genetics:

A:Introns: 51/3; 110/3; 129/1; 436/3
C:Superfamily: Rhizopus glucan 1,4-alpha-glucosidase; glucan 1,4-alpha-glucosidase ho
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
E:1-25/Domain: signal sequence #status predicted <SIG>
E:26-604/Product: glucan 1,4-alpha-glucosidase (Gluc 1) #status predicted <GLI>
E:334-138/Domain: glucoamylase starch-binding domain homology <SBD>
F:116-604/Product: (or 110-604) glucan 1,4-alpha-glucosidase (Gluc 3) #status predict
F:138-604/Product: glucan 1,4-alpha-glucosidase (Gluc 2) #status predicted <GI2>
F:166-592/Domain: glucan 1,4-alpha-glucosidase homology <GAG>

Query Match 15.2% Score 159.3: DB 1: Length 604:
Best Local Similarity 16.0% Pred. No. 21:
Matches 69; Conservative 25; Mismatches 70; Indels 267; Gaps 17;

OY 13 YF-----YSYWDNDHG-----VTYNGPGGFSVNW 39
 || |::| |::| |::|
Db 18 YFLSVLSAASPSSASYOLDSDNYDGSTFGSKTYVKMIAYSKVTYIADG-----SDNW 72
OY 40 SNSGNFVGCKKMP--GTKKNVINFGSSYN-----67
 |::||:| |::| |::|
Db 73 NNNNGNTIAASYASAPISGSNEYWTFPSASINGIKEFYIKYEVSCKTYDDNNSANYOVSTS 132
OY 68 -----PNENSYLS-----75
 |::||:| |::| |::|
Db 133 KPTTTTATTATTAPSTSTTPPPSSSEPAITFPNTSNITSIMIKKEBISRFAHRLRNTP 192
OY 76 -----VYGWSRNPLI-----EX-----YIVENFG 94
 |::||:| |::| |::|
Db 193 GSATGFTLAASLTAGPDYYAAWTRDALTSNVIVIEYENTLTSGNKTIILNLKDVPFSVK 252
OY 95 TYNSTGATKIGE--VISDSVY-----DIYTORVNOPSI 129
 |::| |::| |::| |::|
Db 253 TOSTSYVCNCLEGEKKFNEDGGGYGANGRPONDGPAERATFILFADSYLTORKDASYVT 312
OY 130 GT---ATF-----YOY-----SVRR 142
 |::| |::| |::|
Db 313 GTLKRAIFKDLIDYVWNWNSCGFDLMEEVNGVFHTLLMWARKGILLGADPAKRKGSDTRA 372
OY 143 NHRSSGSVNTANH-----NAWAQ--OGILT-----LGTDNDYOIVAV 176

DB 373 STYSSSTASTIANKISSFWVSNMNIQSVTGVSCKGLDVTLLAANIGSYD----- 426
QY 177 EGFSSGSASI 187
DB 427 DGFPTPGSEKI 437

RESULT 50

G86797
Prophage pi3 protein 09 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: G86797

R:Holstein, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A:Reference number: AB6625; MUID:21235186; PMID:1137471

A:Accession: G86797

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-810 <STO>

A:Cross-references: GB:AE005176; PID:g12724369; PIDN:AAK05481.1; GSPDB:GND00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: pi309

Query Match 15.18; Score 157.7; DB 2; Length 810;

Best Local Similarity 14.78; Pred. No. 45;

Matches 61; Conservative 32; Mismatches 60; Indels 263; Gaps 17;

QY 2 TTOPGTGVNN-----GYFYSY-----WNDGHGCVTYTNGP 31
DB 400 TTAAPTGWINSVPSLVKGOYLTWYTSDTTSETGYSVTYIAKDGNDGIAKDG 459
QY 32 G-----GQFSVMNSNSGNFVGKGW----- 51
DB 460 GIKTTITFYAG-----STSGTAPSSGNATVPVTAAGSYLWTKTWMAITDNTSETGYS 513
QY 52 -----QPGTK--NKVIN-----FSG-----SYNPG 70
DB 514 VAKMGNNGATGPGGPPGSGNDPGKIVSNTEPTTRFKGLTWKXI GMSDLTASDGTVIKPN 573
QY 71 NSYLSVYGMSRNPLIEYIVENFGTYNPSTGATKLGCVTS DGSVDIYRTQVNPSP 129
DB 574 EYYINGTHM---VINFFSVNNFAES-----ITS-----KIDAKNLI 609
QY 130 -----GTATFYQYWSVRNH-----RSSGSVNTANHFNAQAQ----- 163
DB 610 TDGEFVSTTNGPVVTST-----EIKDNHIAISKTDGYVTKNDLAVDTEQGFAMKFTNN 664
QY 164 ----- 163
DB 665 TTGLTREASVNFQGVSTSDSNGNYAQLTPQGTKLSTDPVNTITRSSGVGTSGLRARIN 724
QY 164 -----LTGLTMDYQIYAVEGY-----FSSGS---ASITV 189
DB 725 NGVFYAQSKDVTIPSTAPNSIITIGTMSKFSKFSVSGFDLGLLYSIGQLSVASVTV 780

Search completed: July 1, 2003, 11:49:09
Job time : 44 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 11:47:35 ; Search time 11 Seconds

(without alignments)
716.409 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTGYNGYFYSYWD.....YQIVAVEGYSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt-40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	100.0	222	1 XYN2_TRIRE	P36217 trichoderma
2	990	94.7	190	1 XYN_TRIHA	P48793 trichoderma
3	684.9	65.5	225	1 XYN1_EMENI	P55332 emericella
4	676.9	64.8	225	1 XYNB_ASPAK	P48824 aspergillus
5	670.9	64.2	221	1 XYN2_EMENI	P55333 emericella
6	664.9	63.6	225	1 XYN2_ASPNG	P55330 aspergillus
7	650.9	62.3	221	1 XYN1_COCCA	O06562 cochlodolu
8	635.9	60.9	225	1 XYN1_THELA	O43097 thermomyces
9	614.9	58.8	227	1 XYN1_HUMIN	P55334 humicola in
10	600.4	57.5	335	1 XYNB_STRELO	P26515 streptomyc
11	577.5	55.3	644	1 XYN2_CELFI	P54865 cellulomona
12	572.7	54.8	233	1 XYN2_MAGCR	P55335 magnaporthe
13	568.3	54.4	197	1 XYN1_SCHCO	P35809 schizopyll
14	533.2	51.0	240	1 XYN1_STRLI	P26220 streptomyc
15	528.3	50.6	210	1 XYNB_BACST	P45705 bacillus st
16	506.2	48.4	213	1 XYNB_BACST	P18429 bacillus su
17	505.2	48.3	213	1 XYNB_BACCI	P09650 bacillus ci
18	466.6	44.7	228	1 XYNB_BACPU	P00654 bacillus pu
19	458.7	43.9	261	1 XYNB_CLOSA	P17137 clostridium
20	448.8	42.9	512	1 XYNB_CLOSR	P33538 clostridium
21	446.9	42.8	229	1 XYN1_TRIRE	P36218 trichoderma
22	434	41.5	211	1 XYN1_ASPNG	P55338 aspergillus
23	434	41.5	211	1 XYN1_ASPNG	P55339 aspergillus
24	432	41.3	211	1 XYN1_ASPNG	P55331 aspergillus
25	430.9	41.2	211	1 XYN1_ASPNG	P33557 aspergillus
26	410	39.2	954	1 XYNB_RUMFL	P29126 rumiilococu
27	392.5	37.6	802	1 XYNB_RUMFL	O53317 rumiilococu
28	316.1	30.2	607	1 XYNB_NEOPA	P29127 neocallimas
29	299.3	28.6	608	1 XYNB_FIBSU	P35811 fibrobacter
30	267.3	25.6	625	1 XYNB_PIRSP	O12667 pitomyces s
31	163.6	15.7	666	1 MUR2_ENTHR	P39046 enterococu
32	155.3	14.9	776	1 ISOA_PSEAY	P10342 pseudomonas
33	155.3	14.9	776	1 ISOA_PSEAY	P26501 pseudomonas

34	153.3	14.7	604	1 AMYG_RHIOA	P07683 rhizopus or
35	151	14.4	987	1 YD94_METJA	O58789 methanococ
36	147.4	14.1	699	1 CH11_BACCI	P20533 bacillus ci
37	143.7	13.8	890	1 BCN5_CLOPE	P08696 clostridium
38	143.5	13.7	1196	1 AMYB_PAEPO	P21543 paenibacill
39	142.2	13.6	878	1 FIMD_ECOLI	P30130 escherichia
40	141.4	13.5	1341	1 VGS7_BPT2	P07067 bacterioph
41	140.6	13.5	969	1 SACS_STRSL	O5242 streptococ
42	140.1	13.4	366	1 OM3A_RHILV	O05811 rhizobium
43	139.8	13.4	1953	1 BIGA_SALTY	P25927 salmonella
44	139.7	13.4	2334	1 WAPA_BACSU	O07833 bacillus su
45	139.4	13.3	941	1 GUN_BACSU	P19424 bacillus sp

ALIGNMENTS

RESULT 1	ID	XYN2_TRIRE	STANDARD:	PRT:	222 AA.
AC	P36217:				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)				
DE	(1,4-beta-D-xylan xylanohydrolase 2).				
GN	XYN2				
OS	Trichoderma reesei (Hypocrea jecorina).				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Hypocreales; Hypocreaceae; Hypocrea.				
OX	NCBI_TaxID=51453;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=C30;				
RX	MEDLINE=93103679; PubMed=1369024;				
RA	Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkknen N.,				
RA	Harkki A., Kubicek C.P.;				
RT	"The two major xylanases from Trichoderma reesei: characterization of				
RT	both enzymes and genes."				
RL	Biotechnology 10:1461-1465(1992).				
RN	[2]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=94283373; PubMed=8013449;				
RA	Toerrien A., Rouvinen J.;				
RT	"three-dimensional structure of endo-1,4-beta-xylanase II from				
RT	Trichoderma reesei: two conformational states in the active site."				
RL	EMBO J. 13:2493-2501(1994).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=95127663; PubMed=7827044;				
RA	Toerrien A., Rouvinen J.;				
RT	"Structural comparison of two major endo-1,4-xylanases from				
RT	Trichoderma reesei."				
RL	Biochemistry 34:847-856(1995).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=96302263; PubMed=8755744;				
RA	Havulinainen R., Toerrien A., Laitinen T., Rouvinen J.;				
RT	"Covalent binding of three epoxalykyl xylotides to the active site of				
RT	endo-1,4-xylanase II from Trichoderma reesei."				
RL	Biochemistry 35:9617-9624(1996).				
CC	-1- CATALYTIC ACTIVITY: Endohydrolase of 1,4-beta-D-xylosidic				
CC	linkages in xylans.				
CC	-1- PATHWAY: Xylan degradation.				
CC	-1- PTM: THE N-TERMINUS IS BLOCKED.				
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL				
CC	HYDROLASES).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation ;				

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/> or send an email to license@ebi.ac.uk).

EMBL: X69573; CAA49293.1; -
PIR: S39154; S39154.
PDB: 1XVO: 08-AUG-95.
PDB: 1XYP: 08-AUG-95.
PDB: 1ENR: 08-AUG-95.
PDB: 1RED: 11-JAN-97.
PDB: 1REE: 11-JAN-97.
PDB: 1REF: 11-JAN-97.
InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
K1 xylan degradation; Hydrolase; Glycoprotein; Signal;
3D-structure.
FT SIGNAL 1 32
FT CHAIN 33 222 ENDO-1,4-BETA-XYLANASE 2.
FT ACT_SITE 118 118 NUCLEOPHILE.
FT CARBOHYD 209 209 PROTON DONOR.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 222 AA; 24172 MW; 15F7032FACF9636F CRC64;

Query Match 100.0%; Score 1045; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 2,7e-39;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTTIPGTGYNNGYYSYWNDDGCVTNTNGGQFSYVMSNSGNGFVGKGMQPTKKKVI 60
DB 33 OTTIPGTGYNNGYYSYWNDDGCVTNTNGGQFSYVMSNSGNGFVGKGMQPTKKKVI 92
QY 61 NFSGSYNPNNGSYLSYVGWSRNPLEYIYVENFGTYPNPGATKLGCVTSDGSYYDIYRT 120
DB 93 NFSGSYNPNNGSYLSYVGWSRNPLEYIYVENFGTYPNPGATKLGCVTSDGSYYDIYRT 152
QY 121 ORVNPSTIGATPYQWVSVRNRHSSGSVNTANHFANMAOGLTGTMDYQIYAVGCGYF 180
DB 153 ORVNPSTIGATPYQWVSVRNRHSSGSVNTANHFANMAOGLTGTMDYQIYAVGCGYF 212
QY 181 SSGSASITVS 190
DB 213 SSGSASITVS 222

RESULT 2
XYN1_TRIHA
ID XYN1_TRIHA STANDARD; PRT; 190 AA.
AC P48793;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
xylanohydrolase).
OS Trichoderma harzianum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; mitosporic Hypocreales; Trichoderma.
OX NCBI_TaxID=5544;
RN [1]
RP SEQUENCE.
RC STRAIN=ES8;
RA Yaguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,
RA Saddler J.N.;
RT "The amino acid sequence of the 20 kD xylanase from Trichoderma
harzianum ES8".
RL (in) Visser J., Beldman G., Kusters-van Someren M.A.,
Voragen A.G.J. (eds.);

RL xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,

RA Yaguchi M.;

RT "High-resolution structures of xylanases from B.circulans and

RT T.harzianum identify a new folding pattern and implications for the

RT atomic basis of the catalysis.";

RL (in) Suomenen P., Reinkainen T. (eds.);

RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,

RL Foundation for Biotechnical and Industrial Fermentation Research,

RL Helsinki (1993).

CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

CC linkages in xylans.

CC -1 PATHWAY: Xylan degradation.

CC -1 SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL

CC HYDROLASES)

PDB: 1XND: 20-DEC-94.

DR InterPro: IPR001137; GH_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLHYDRASE1.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

K1 xylan degradation; Hydrolase; Glycosidase; 3D-structure.

FT ACT_SITE 86 86 NUCLEOPHILE.

FT ACT_SITE 177 177 PROTON DONOR.

SEQUENCE 190 AA; 20703 MW; 6A0F4D1C3599C698 CRC64;

Query Match 94.7%; Score 990; DB 1; Length 190;
Best Local Similarity 94.2%; Pred. No. 5.1e-37;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTTIPGTGYNNGYYSYWNDDGCVTNTNGGQFSYVMSNSGNGFVGKGMQPTKKKVI 60
DB 1 OTTIPGTGYNNGYYSYWNDDGCVTNTNGGQFSYVMSNSGNGFVGKGMQPTKKKVI 60
QY 61 NFSGSYNPNNGSYLSYVGWSRNPLEYIYVENFGTYPNPGATKLGCVTSDGSYYDIYRT 120
DB 61 NFSGSYNPNNGSYLSYVGWSRNPLEYIYVENFGTYPNPGATKLGCVTSDGSYYDIYRT 120
QY 121 ORVNPSTIGATPYQWVSVRNRHSSGSVNTANHFANMAOGLTGTMDYQIYAVGCGYF 180
DB 121 ORVNPSTIGATPYQWVSVRNRHSSGSVNTANHFANMAOGLTGTMDYQIYAVGCGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
XYN1_EMENT
ID XYN1_EMENT STANDARD; PRT; 225 AA.
AC P55332; 000173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
DE (1,4-beta-D-xylan xylanohydrolase 1).
OS Emeritella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emeritella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96236210; PubMed=8787417;
RA Perez-Gonzalez J.A., de Graaf L.H., Visser J., Ramon D.;
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
RT Aspergillus nidulans xylanase genes.";
RL Appl. Environ. Microbiol. 62:2179-2182(1996).
CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1 PATHWAY: Xylan degradation.
CC -1 SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL

CC HYDROLASES).

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: Z49892; CA90073.1; -

CC DR HSSP: P48793; 1XND.

CC DR InterPro: IPR001137; GH_11.

CC DR Pfam: PF00457; Glyco_hydro_11; 1.

CC DR PRINTS: PR00911; GLYHIDRLASE1.

CC DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

CC DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

CC KM Xylan degradation; Hydrolase; Glycosidase; Signal.

CC FT CHAIN 1 19 POTENTIAL.

CC FT ACT_SITE 121 121 ENDO-1,4-BETA-XYLANASE 1.

CC FT ACT_SITE 212 212 NUCLEOPHILE (BY SIMILARITY).

CC FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).

CC SQ SEQUENCE 225 AA: 24070 MW: 670F2C79602C7ECC CRC64;

Query Match 65.5%; Score 684.9; DB 1; Length 225;

Best Local Similarity 66.1%; Pred. No. 1.5e-23;

Matches 121; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGYNNGFFSYWMDHGCVTYTNGPGQFSVNMNSNGNFVGKMGWPGTKNKVINFSGSY 66

Db 43 TGENNGYYYSFMTDGGDVTYTNAGSGSYVMSNGNFVGKMGWPGSA-KDITYSGNF 101

QY 67 NPNNGSYLYSGSRNPDIETVYENGTYNPSTGATKLGCVTSDGSYDIYRTQRYNOP 126

Db 102 NPGNGYLYSGYGTWTPDIETVYEVESIGTNPSSGQHRGTYSDDGFTDIYATRTNAP 161

QY 127 SIIGTATFYQYWSVRNRHSSGSSVNTANHFNAAGGLTGTDYQIYAVEGFSSGSAS 186

Db 162 SIIGTATFYQYWSVRNRHSSGSSVNTANHFNAAGGLTGTDYQIYAVEGFSSGSAS 221

QY 187 ITV 189

Db 222 ITV 224

RESULT 4

XYNB_ASPAK STANDARD; PRT; 225 AA.

AC P48824;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)

DE (1,4-beta-D-xylan xylanohydrolase B).

GN XYNB.

OS Aspergillus awamori (var. kawachi).

OC Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX NCBI_TaxID=40384;

RN (1)

RP SEQUENCE FROM N.A.

RA STRAIN=IFO 4308;

RC Ito K.;

RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

CC linkages in xylans.

CC -1- PATHWAY: Xylan degradation.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL

CC HYDROLASES).

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: D38070; BAA07264.1; -

CC DR HSSP: P36217; 1XVO.

CC DR InterPro: IPR001137; GH_11.

CC DR Pfam: PF00457; Glyco_hydro_11; 1.

CC DR PRINTS: PR00911; GLYHIDRLASE1.

CC DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

CC DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

CC KM Xylan degradation; Hydrolase; Glycosidase; Signal.

CC FT CHAIN 1 18 POTENTIAL.

CC FT ACT_SITE 121 121 ENDO-1,4-BETA-XYLANASE B.

CC FT ACT_SITE 212 212 NUCLEOPHILE (BY SIMILARITY).

CC FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).

CC SQ SEQUENCE 225 AA: 24146 MW: 54B13D48AF5C7115 CRC64;

Query Match 64.8%; Score 676.9; DB 1; Length 225;

Best Local Similarity 66.1%; Pred. No. 3.3e-23;

Matches 121; Conservative 23; Mismatches 38; Indels 1; Gaps 1;

QY 7 TGYNNGFFSYWMDHGCVTYTNGPGQFSVNMNSNGNFVGKMGWPGTKNKVINFSGSY 66

Db 43 TGENNGYYYSFMTDGGDVTYTNAGSGSYVMSNGNFVGKMGWPGSA-KDITYSGNF 101

QY 67 NPNNGSYLYSGSRNPDIETVYENGTYNPSTGATKLGCVTSDGSYDIYRTQRYNOP 126

Db 102 NPGNGYLYSGYGTWTPDIETVYEVESIGTNPSSGQHRGTYSDDGFTDIYATRTNAP 161

QY 127 SIIGTATFYQYWSVRNRHSSGSSVNTANHFNAAGGLTGTDYQIYAVEGFSSGSAS 186

Db 162 SIIGTATFYQYWSVRNRHSSGSSVNTANHFNAAGGLTGTDYQIYAVEGFSSGSAS 221

QY 187 ITV 189

Db 222 ITI 224

RESULT 5

XYN2_EMENTI STANDARD; PRT; 221 AA.

AC P55333; 000176;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)

DE (1,4-beta-D-xylan xylanohydrolase 2).

OS Emericella nidulans (Aspergillus nidulans).

OC Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; Emericella.

OX NCBI_TaxID=5072;

RN (1)

RP SEQUENCE FROM N.A.

RA MEDLINE=96236210; PubMed=8787417;

RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;

RT "Molecular cloning and expression in *Saccharomyces cerevisiae* of two

RT Aspergillus nidulans xylanase genes.";

RL Appl. Environ. Microbiol. 62:2179-2182(1996).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

CC linkages in xylans.

CC -1- PATHWAY: Xylan degradation.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL

CC HYDROLASES).

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

```

CC -----
DR EMBL: Z49893; CA90074.1; -.
DR HSSP: P48793; 1XND.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro.11; 1.
DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR KXylan degradation: Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 18
FT CHAIN 19 221
FT ACT_SITE 117 117
FT ACT_SITE 208 208
FT ACT_SITE 221 AA; 23517 MW; 42665E80DDE9475 CRC64;
SQ SEQUENCE 221 AA; 23517 MW; 42665E80DDE9475 CRC64;

Query Match
Best Local Similarity 64.2%; Score 670.9; DB 1; Length 221;
Matches 121; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

OY 7 TGYNNGFYSYWNDHGVVTYTNPGGQFVSVMNSNGNFVGKMGQPKRKVIINFGSGY 66
DB 39 TGTSGGYYSFMTDGGDVYTTNGDGGSYTEVETKGVNFVGKMGWPGS-SQTISYSGSF 97
OY 67 NPNGNSYLSVYGWGRNPLIEYIYENFGTYNPSGATKRLGEVTSDGSVYDIYTRQRYNP 126
DB 98 TPGSGYLSVYGWQNPILIEYIYESYGDYNPAGTGHQGLSDGSTYDIYTRATRENAP 157
OY 127 SIIGTAFYQYWSYRNHRSSGSVNTANHFNAMAQGLTLGTMDOYQIYAVEGYFSSGSAS 186
DB 158 SIETATFTQYWSYRQKRTSGSVTTQNHFDAMSQGLTGHNTQIYAVEGYOSSGSAS 217
OY 187 ITVS 190
DB 218 ITVS 221

RESULT 6
XYN2_ASPNG STANDARD: PRT; 225 AA.
ID XYN2_ASPNG
AC P55330; Q12557;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE (1,4-beta-D-xylan xylanohydrolase II).
GN XYNB.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4066;
RA Ito K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: Xylan degradation..
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D38071; BAA07265.1; -.
DR HSSP: P09850; 1XNB.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro.11; 1.

```

```

DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR KXylan degradation: Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 18
FT PROPEP 19 37
FT CHAIN 38 225
FT ACT_SITE 121 121
FT ACT_SITE 212 212
FT ACT_SITE 225 AA; 24057 MW; CAB8BB007AB2B8ED CRC64;
SQ SEQUENCE 225 AA; 24057 MW; CAB8BB007AB2B8ED CRC64;

Query Match
Best Local Similarity 63.6%; Score 664.9; DB 1; Length 225;
Matches 120; Conservative 22; Mismatches 40; Indels 1; Gaps 1;

OY 7 TGYNNGFYSYWNDHGVVTYTNPGGQFVSVMNSNGNFVGKMGQPKRKVIINFGSGY 66
DB 43 TGENNGFYSFMTDGGDVYTTNDAGAYVEMSWNFVGKMGWPGSAD-ITVSGTF 101
OY 67 NPNGNSYLSVYGWGRNPLIEYIYENFGTYNPSGATKRLGEVTSDGSVYDIYTRQRYNP 126
DB 102 TPGSGYLSVYGWTTDLIEYIYESYGDYNPAGTGHQGLSDGSTYDIYTRATRENAA 161
OY 127 SIIGTAFYQYWSYRNHRSSGSVNTANHFNAMAQGLTLGTMDOYQIYAVEGYFSSGSAS 186
DB 162 SIOTATFTQYWSYRQKRVGVTYTNHFNAMAQGLTGHNTQIYAVEGYOSSGSAS 221
OY 187 ITV 189
DB 222 ITV 224

RESULT 7
XYN1_COCCA STANDARD: PRT; 221 AA.
ID XYN1_COCCA
AC Q06562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYL1.
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Race 1 / Isolate SB111;
RC MEDLINE=94003417; PubMed=8400376;
RA Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT "Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase
RT gene from the maize pathogen Cochliobolus carbonum."
RL Mol. Plant Microbe Interact. 6:467-473(1993).
RN [2]
RP PARTIAL SEQUENCE.
RA Holden F.R., Walton J.D.;
RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum."
RL Physiol. Mol. Plant Pathol. 40:39-47(1992).
CC -1- FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE
CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-
CC WALLS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```



```
CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X76047; CAA53632.1; -
DR HSSP: Q43097; 1YNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro.11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation: Hydrolase; Glycosidase; Signal.
KW SIGNAL
FT CHAIN 1 19
FT ACT_SITE 20 227 ENDO-1,4-BETA-XYLANASE 1.
FT ACT_SITE 121 121 NICLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 227 AA; 25601 MW; 5C2FE6ADCEADAIF CRC64;

Query Match 58.8%; Score 614.9; DB 1; Length 227;
Best Local Similarity 58.8%; Pred. No. 1.7e-20;
Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

OY 8 GYNNGYFYSYNDGCGVYTYNGPGGQFSVMNSNGNFVGKGWPGTKRNKYNFSGSYN 67
DB 44 GHHNNGFYSSMSDGGGOVYTNLEGRYQVRNRTNGNFVGGKGNPPT-GRTINYGCFN 102
OY 68 PNGNSYLSVYGWSRNPLEYIVENFGTYNPSTGATKGEVTSQGSVDIYRTQVNPSPS 127
DB 103 POGNCTYLAIVGTRNPLVEYIEYIEGYTYNPGSCAQVGYTTRDDQYDFVSTRYNOPS 162
OY 128 IIGTATFYQVYSVRNRHSSGSVNTANFNHMAAOGTLTGMDQIYAVEGYFSSGSASI 187
DB 163 IDGTRTFQOYWSIRKNRKGVSVMNQNHFNMAOQGMPLGQHYGVAVTEGYSGSGESDI 222
OY 188 TV 189
DB 223 YV 224

RESULT 10
XYNB_STRLI STANDARD; PRT; 335 AA.
AC P26515;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B).
GN XLNB.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT *Sequences of three genes specifying xylanases in Streptomyces
RT lividans.*;
RL Gene 107:75-82(1991).
RN [2]
RP REVISIONS TO 29-32 AND 252-307.
RC STRAIN=66 / 1326;
```

```
RX MEDLINE=95189090; PubMed=7533741;
RA Shareck F., Biely P., Morosoli R., Kluepfel D.;
RT *Analysis of DNA flanking the xlnB locus of Streptomyces lividans
RT reveals genes encoding acetyl xylan esterase and the RNA component of
RT ribonuclease P.*;
RL Gene 153:105-109(1995).
RN [3]
RP REVISION TO 225.
RA Shareck F.;
CC -1- FUNCTION: CONTRIBUTES TO the EMBL/Genbank/DBJ databases.
CC -1- COMPONENT OF PLANT CELL-WALLS. XLNA AND XLNB SEEM TO ACT
CC SEQUENTIALLY ON THE SUBSTRATE TO YIELD XYLULOSE AND XYLULOSE
CC AS CARBON SOURCES.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M64552; AAC06114.2; -
DR HSSP: P09850; 1XNB.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro.11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation: Hydrolase; Glycosidase; Signal.
KW SIGNAL
FT CHAIN 1 41
FT ACT_SITE 42 335 ENDO-1,4-BETA-XYLANASE B.
FT DOMAIN 42 230 CATALYTIC.
FT DOMAIN 231 249 LINKER ("HINGE") (GLY-RICH BOX).
FT DOMAIN 250 335 XYLAN-BINDING (POTENTIAL).
FT ACT_SITE 128 128 NICLEOPHILE (BY SIMILARITY).
FT ACT_SITE 218 218 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 335 AA; 35575 MW; 513B1458BF8FCF CRC64;

Query Match 57.5%; Score 600.4; DB 1; Length 335;
Best Local Similarity 55.1%; Pred. No. 1.5e-19;
Matches 109; Conservative 32; Mismatches 41; Indels 16; Gaps 5;

OY 5 PGT-----GYNNGFYSYNDGCGVYTYNGPGGQFSVMNSNGNFVGKGWQ 52
DB 36 PGTAAQADIVYTTNDEGINNGYISFWTDSCGTVMNMGSGQYSTSRKNTGNFPAAGGWA 95
OY 53 PGTNNKYNINSGSYNPNNGNSYLSVYGWSRNPLEYIVENFGTYNPSTGATKGEVTSDG 112
DB 96 NGGR-RTVQYSGSPENPGNAVALYLGWTSNPLVEYIYDMNGTYRP-TGEYK-GTYVSDG 152
OY 113 SVYDIYTORYNOSIIGTATFYQVYSVRNRHSSGSVNTANFNHMAAOGTLTGMD-Y 171
DB 153 GTYDIYITTRNKRKSVSGTRTFDDQYWSVRKRTGRTTGNHFDAMRAGMPLGNFSY 212
OY 172 QIYAVEGYFSSGSASITY 189
DB 213 MIMATBEGYSGSSSINV 230

RESULT 11
XYND_CELFI STANDARD; PRT; 644 AA.
AC P54865;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
```

OY	127	SIIG-TATFYQVYSVRNRHSSGSVNTANHFNAAGCGLTGMDYOIVAVEGFSSGSA	185
D6	165	SIEDSGSTFYYQSVYRPOQRKFGTGTISGNHFDMAASKMNLGRNNYMIMATEGYSSGSS	224
OY	186	SITVS 190	
D6	225	SITVS 229	

		RESULT 12	
ID	XYN2_MAGCR	STANDARD.	PRT; 233 AA.
AC	P53335; Q01171;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)		
DE	(1,4-beta-D-xylan xylanohydrolase 22).		
GN	XYN2.		
OS	Magnaporthe grisea (Rice blast fungus) (Piricularia grisea).		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
CC	Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthe.		
OX	NCB1_TaxID=148305;		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN-KEN60-19;		
RX	MEDLINE=96172742; PubMed=8589407;		
RA	Wu S.C., Kaufman S., Darvill A.G., Albersheim P.:		
RT	"Purification, cloning and characterization of two xylanases from		
RL	Magnaporthe grisea, the rice blast fungus."		
CC	Mol. Plant Microbe Interact. 8:506-514(1995).		
CC	-I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylousidic		
CC	linkages in xyans.		
CC	-I- PATHWAY: Xylan degradation.		
CC	-I- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL		
CC	HYDROLASES).		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@sib-sib.ch).		
CC	-----		
DR	EMBL: L37529; AAC41683.1; .		
DR	HSSP: O43097; IYNA.		
DR	InterPro: IPR001137; GH_11.		
DR	Pfam: PF00457; Glyco_hydro_11; 1.		
DR	PRINTS: PR00911; GLHYDRASE11.		
DR	PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.		
KW	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.		
DM	Xylan degradation; Hydrolase; Glycosidase; Signal.		
FT	SIGNAL 1 39		
FT	CHAIN 40 233		
FT	ACT_SITE 126 126		
FT	ACT_SITE 217 217		
FT	SEQUENCE 233 AA; 25491 MW; 400963836F581F98 CRC64;		
	Query Match	54.8%; Score 572.7; DB 1; Length 233;	
	Best Local Similarity	51.8%; Pred. No. 1.3e+18;	
	Matches	99; Conservative 35; Mismatches 54; Indels 3; Gaps 2;	
OY	1	QTDPGTGYNNGEFYSYWNDDGHGVYTYNGPGQSPYSVMWSNGNFVGSKMQPGTKNKVI	60
D6	40	QSTPSSTGRHGNYGYYSMTDGASPFQYQVONCGNGSGSYSVOMSGNFVGSKGMWP-GSKSI	98
OY	61	NFSGSYNN--NGSNLSLYYGSGMRPLLEYTVLVENNGTFNPSTGATKLGLEVISDSQVDYI	118
D6	99	TYSGFNVNNGNALCYLGYTNQMLVEYLLYLELVLENTEGENTPNSQSORSRTLOAAGCTYTLH	158
OY	119	RTQRNQPSIIIGTATFYQVYSVRNRHSSGSVNTANHFNAAGCGLTGMDYOIVAVEG	178

Db 159 ESTRNQPSIEGRTFRQOYWAIRQKRNKSGTNTGFEQWEMERAGKRMGNHNMIVATEG 218
QY 179 YFSSGSASITV 189
Db 219 YRSAGNSINIV 229

RESULT 13
XVNA_SCHCO STANDARD: PRT: 197 AA.

AC P35809;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
Xylanohydrolase A).
GN XVNA.
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;
RN [1]
RP SEQUENCE.
RC STRAIN-ATCC 38548 / Delmar;
RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.;
RL (in) Visser J., Beidman G., Kusters-van Someren M.A.,
RL Vorgen A.G.J. (eds.);
RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
RN [2]
RP SEQUENCE, AND DISULFIDE BONDS.
RC STRAIN-ATCC 38548 / Delmar;
RX MEDLINE=94063044; PubMed=8243636;
RA Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
RA Jurasek L., Palce M.G.;
RT "Amino acid sequence and thermostability of xylanase A from
RT Schizophyllum commune";
RT FEBS Lett. 334:296-300(1993).
RN [3]
RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.
RC STRAIN-ATCC 38548 / Delmar;
RX MEDLINE=94155888; PubMed=7906649;
RA Bray M.R., Clarke A.J.;
RT "Identification of a glutamate residue at the active site of xylanase
RT A from Schizophyllum commune";
RT Eur. J. Biochem. 219:821-827(1994).
CC -1- FUNCTION: HYDROLYSES XYLANS INTO XYLOBIOSE AND XYLOSE. THIS
CC -1- XYLANASE HAS A VERY BROAD PH ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC PIR: S38973; S38973.
CC PIR: A44597; A44597.
CC HSSP: O43097; LYNA.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC KXylan degradation; Hydrolase; Glycosidase.
FT ACT_SITE 87
FT ACT_SITE 184
FT DISULFID 111 160
FT PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 197 AA; 20978 MW; 42C8074E67C1FBE9 CRC64;

Query Match 54.4%; Score 568.3; DB 1; Length 197;
Best local Similarity 55.0%; Pred. No. 1.4e-18;
Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

7 TGTNGGYFSYWNDSHGAVTYTNGPGGQPSVWMS-NSGNFVGKGMQPGTKNKVINFSGS 65

Db 7 TGTGCGYYSWMTDGAADATYQNGGSGSYTLTMSGNNGULYGGKGNPCAAARSISYST 66
QY 66 YNPNGNSYLSVYGSWNRNPLEIYVENFGTYNPSTGATKLGVTSDGSYDIYRQVRVQ 125
Db 67 YQPNNGNSYLSVYGSWNRNPLEIYVENFGTYNPSTGATKLGVTSDGSYDIYRQVRVQ 126
QY 126 PSTIGTATFYQWVSVRNRHRS-----SGSVNTHNHNMAAOGTLTGT-MDYQIVAVEG 179
Db 127 PSTIGTATFYQWVSVRNPKKAPGSGISGTVDVQCHPDAMKGLAMNLGSEHNTQIVATEG 186
QY 180 FSSGSASITVS 190
Db 187 QSSGSTATIVT 197

RESULT 14
XVNC_STRLI STANDARD: PRT: 240 AA.

AC P26220;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
DE (1,4-beta-D-xylan xylanohydrolase C).
GN XLNC.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
RC STRAIN-66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Sharack F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RT lividans";
RT Gene 107:75-82(1991).
RL -1- FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE MAJOR
RL COMPONENT OF PLANT CELL-WALLS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M64553; AAA26836.1; -
CC EMBL: A25307; CAA01768.1; -
CC PIR: JS0591; JS0591.
CC HSSP: P09850; IXNB.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC KXylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 49
FT CHAIN 50 240
FT ACT_SITE 134 134
FT ACT_SITE 226 226
FT PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;

Query Match 51.0%; Score 533.2; DB 1; Length 240;
Best local Similarity 50.5%; Pred. No. 7.1e-17;

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler H., Weitzengger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zurcher A.,
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
RT *subtilis*.";
RN Nature 390:249-256(1997).
RN (4)
RP MUTAGENESIS.
RA Makarchuk W., Method N., Lanthier P., Sung W., Selby V., Yaguchi M.,
RA To R., Campbell R., Rose D., Kusters-van Someren M.A.,
RL (In) Visser J., Belman G.,
RL Voragen A.G.J. (eds.);
RL xylans and xylanases, pp.439-442, Elsevier, Amsterdam (1992).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M36648; AAA22897.1; -
CC EMBL: AF027868; AAB84458.1; -
CC EMBL: 289114; CAB3776.1; -
CC PIR: S3157; S3157.
CC DR HSP: P09850; 1XNB.
CC DR Subtilist; BG10808; xyna.
CC DR InterPro: IP001137; GH_11.
CC DR Pfam: PF00457; Glyco_hydro_11; 1.
CC DR PRINTS: PR00911; GLHYDRASE1.
CC DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC KM xylan degradation: Hydrolase; Glycosidase; Signal; Complete proteome.
CC FT CHAIN 1 29 213
CC FT ACT_SITE 106 106
CC FT ACT_SITE 200 200
CC FT MUTAGEN 106 106
CC FT MUTAGEN 200 200
CC SEQUENCE 213 AA: 23345 MW: 20CBA35238CC0564.CRC64;
Query Match 48.4%; Score 506.2; DB 1; Length 213;
Best Local Similarity 53.8%; Pred. No. 8, 6e-16;
Matches 98; Conservative 29; Mismatches 47; Indels 8; Gaps 6;
OY 14 FYSYVNDHGCVYTYNGPGGFSVNMNSGNFVGKQWPGTKNKVINF-SCSYNPNGNS 72
DB 33 YQNMWTDGCGIYVNAVNGSGNYSVNMNSGNFVGKQWPGTKNKVINF-SCSYNPNGNS 92
OY 73 YLSYVGMNRNPLEIYVNEFTYNSGATKLGVTSDGSYVDIYRQVNPSTIG-T 131
DB 93 YLTLYGMRSPLEIYVNEFTYNSGATKLGVTSDGSYVDIYRQVNPSTIG-T 150
OY 132 AFYQVWSYRNRHRSQS---VNTANHFNAQAQGLTGT-MDYQVANEVGFSSGSASI 187
DB 151 TTFQVWSYRNRHRSQS---VNTANHFNAQAQGLTGT-MDYQVANEVGFSSGSASI 210
OY 188 TV 189
DB 211 TV 212
RESULT 17
XYNA_BACCI STANDARD: PRT: 213 AA.
AC P09850;

DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (xylanase) (1,4-beta-D-
DE xylan xylanohydrolase).
GN XNA.
OS *Bacillus* circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1397;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=88303346; PubMed=3405767;
RX Yang R.C.A., Mackenzie C.R., Narang S.A.;
RT "Nucleotide sequence of a *Bacillus* circulans xylanase gene."
RT Nucleic Acids Res. 16:7187-7187(1988).
RN (2)
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS), AND MUTAGENESIS.
RX MEDLINE=94290322; PubMed=8019418;
RA Makarchuk W.W., Campbell R.L., Sung W.L., Davoodi J., Yaguchi M.;
RT "Mutational and crystallographic analyses of the active site residues
RT of the *Bacillus* circulans xylanase."
RL Protein Sci. 3:467-475(1994).
RN (3)
RP STRUCTURE BY NMR.
RX MEDLINE=96322313; PubMed=8756457;
RA McIntosh L.P., Hand G., Johnson P.E., Joshi M.D., Koerner M.,
RA Plesniak L.A., Ziser L., Makarchuk W.W., Withers S.G.;
RT "The pKa of the general acid/base carboxyl group of a glycosidase
RT cycles during catalysis: a 13C-NMR study of *Bacillus* circulans
RT xylanase."
RL Biochemistry 35:9958-9966(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X07723; CAA30553.1; -
CC PIR: S01734; S01734.
CC DR PDB: 1BCX; 15-OCT-94.
CC DR PDB: 1XNB; 20-DEC-94.
CC DR PDB: 1XNC; 20-DEC-94.
CC DR InterPro: IP001137; GH_11.
CC DR Pfam: PF00457; Glyco_hydro_11; 1.
CC DR PRINTS: PR00911; GLHYDRASE1.
CC DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC KM xylan degradation: Hydrolase; Glycosidase; Signal; 3D-structure.
CC FT CHAIN 1 29 213
CC FT ACT_SITE 106 106
CC FT ACT_SITE 200 200
CC SEQUENCE 213 AA: 23359 MW: 4BA0A35238CC0135.CRC64;
Query Match 48.3%; Score 505.2; DB 1; Length 213;
Best Local Similarity 53.8%; Pred. No. 9, 5e-16;
Matches 98; Conservative 28; Mismatches 48; Indels 8; Gaps 6;
OY 14 FYSYVNDHGCVYTYNGPGGFSVNMNSGNFVGKQWPGTKNKVINF-SCSYNPNGNS 72
DB 33 YQNMWTDGCGIYVNAVNGSGNYSVNMNSGNFVGKQWPGTKNKVINF-SCSYNPNGNS 92
OY 73 YLSYVGMNRNPLEIYVNEFTYNSGATKLGVTSDGSYVDIYRQVNPSTIG-T 131
DB 93 YLTLYGMRSPLEIYVNEFTYNSGATKLGVTSDGSYVDIYRQVNPSTIG-T 150


```

OY 132 ATFOYMSVRNRHSSGS---VNTANHNANAQOGLTGT-MDYQIVAVEGYFSSGSASI 187
DB 131 TTFOTYMSVRSKRTGTSNATITTFNNHNANKSHGMNGLSNMAYQVATGEGYSSGSNV 210

OY 188 TV 189
DB 211 TV 212

RESULT 18
XYNA_BACPU STANDARD: PRT; 228 AA.
ID XYNA_BACPU STANDARD: PRT; 228 AA.
AC P00694;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
DE (1,4-beta-D-xylan xylanohydrolase A).
GN XYNA.
OS Bacillus pumilus (Bacillus mesentericus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1408;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-1P0;
RA Fukusaki E., Panbangred W., Shimmyo A., Okada H.;
RT "The complete nucleotide sequence of the xylanase gene (xyna) of
RT Bacillus pumilus."
RL FEBS Lett. 171:197-201(1984).
RN [2]
RN REVISION TO 103.
RA Urabe I.;
RN Submitted (FEB-1991) to the EMBL/Genbank/DBJ databases.
RN [3]
RN MUTAGENESIS, AND ACTIVE SITES.
RP MEDLINE=93075064; PubMed=1359880;
RA Ko E.P., Akatsuka H., Moriyama H., Shimmyo A., Hata Y., Katsube Y.,
RA Urabe I., Okada H.;
RT "Site-directed mutagenesis at aspartate and glutamate residues of
RT xylanase from Bacillus pumilus."
RL Biochem. J. 288:117-121(1992).
RN [4]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=93075064; PubMed=1359880;
RA Hata Y., Moriyama H., Shimmyo A., Okada H., Katsube Y.;
RL Unpublished results, cited by:
RL Ko E.P., Akatsuka H., Moriyama H., Shimmyo A., Hata Y., Katsube Y.,
RL Urabe I., Okada H.;
RL Biochem. J. 288:117-121(1992).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -!- PATHWAY: xylan degradation.
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X00660; CAA25278.1; -
CC PIR: A00848; WBSXP.
CC HSSP: P09850; 1XNB.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW xylan degradation; Hydrolase; Glycosidase; Signal.

```

```

FT SIGNAL 1 27
FT CHAIN 28 228 ENDO-1,4-BETA-XYLANASE A.
FT ACT_SITE 120 120 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 209 209 PROTON DONOR (BY SIMILARITY).
FT MUTAGEN 120 120 E->S: LOSS OF ACTIVITY.
FT MUTAGEN 209 209 E->D: LOSS OF ACTIVITY.
SQ SEQUENCE 228 AA; 25491 MW; 32EF9833E7B5E503 CRC64;

Query Match 44.7%; Score 466.6; DB 1; Length 228;
Best Local Similarity 50.3%; Pred. No. 5,2e-14;
Matches 95; Conservative 25; Mismatches 35; Indels 14; Gaps 5;

OY 8 GYNNGCFYSYWNMDGCVTYTNGPCGQSFVMSNSGNFGGK-----WQGTNKK 58
DB 36 GNHSGDYELMKD-YGNISMTLLNNGAFSAGHNNTGNLFRKGKFDSTRTTHQLG--NI 92
OY 59 VINFSGSYNPNQNSYLSVYSGSRNLEIYIVENEGTYNPSTGATKLGVTSDGSVDIY 118
DB 93 SINYNASENPGNSYLCVYGTQSPFLAEYIIVDSWGTYRP-TGAVK-GSFVADGGTVDIY 150
OY 119 RTQRYNOPSIIIGTATFYQMSVRNRHSSGSVNTANHNANAQOGLTGTMDYQIVAVEG 178
DB 151 ETRRYNOPSIIIGTATFYQMSVRNRHSSGSVNTANHNANAQOGLTGTMDYQIVAVEG 210
OY 179 YFSSGSASI 187
DB 211 YOSSGSANV 219

RESULT 19
XYNA_CLOSA STANDARD: PRT; 261 AA.
ID XYNA_CLOSA STANDARD: PRT; 261 AA.
AC P17137;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
DE xylan xylanohydrolase).
GN XYNB.
OS Clostridium saccharobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxId=169679;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-P262;
RX MEDLINE=90245673; PubMed=2336398;
RA Zappe H., Jones W.A., Woods D.R.;
RT "Nucleotide sequence of a Clostridium acetobutylicum P262 xylanase
RT gene (xynB)."
RL Nucleic Acids Res. 18:2179-2179(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -!- PATHWAY: xylan degradation.
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M31726; AAA23287.1; -
CC PIR: S12745; S12745.
CC HSSP: P36217; 1XYO.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.

```

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.
 KM Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 261
 FT ACT_SITE 152 152
 FT ACT_SITE 242 242
 FT ACT_SITE 261 261
 SQ SEQUENCE 261 AA; 29032 MW; 339C3616F6FD14AE CRC64;
 Query Match 43.9%; Score 458.7; DB 1; Length 261;
 Best Local Similarity 47.1%; Pred. No 1.5e-13;
 Matches 89; Conservative 27; Mismatches 60; Indels 13; Gaps 4;
 QY 8 GYVNGYFYSYWNDHGCVTYTNGPGQFVSVMNSNGNFVGKNGK-----WQPGTKNK 58
 DB 68 GYVNGYFYSYWNDHGCVTYTNGPGQFVSVMNSNGNFVGKNGK-----WQPGTKNK 124
 QY 59 VVIFSSGYNPNNGSYLSYVGMNRNPLEIYIVNEFGTYNPGTATKLGVTSGSYDYI 118
 DB 125 SVNYDCNYPYSGNSYLCYVGMNTPLEIYIVNEFGTYNPGTATKLGVTSGSYDYI 183
 QY 119 RTQVNOPSTIGATFYQYVSVRRNRSSGVSNTANHFNMAOQGLTGMDYQIYAVES 178
 DB 184 ETRINOPSTIGATFYQYVSVRRNRSSGVSNTANHFNMAOQGLTGMDYQIYAVES 243
 QY 179 YFSSGSASI 187
 DB 244 YQSSGKADV 252
 RESULT 20
 XYNL_CLOS
 AC P33558;
 ID XYNL_CLOS STANDARD; PRT; 512 AA.
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
 GN XYNL.
 OS Clostridium stercorarium.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1510;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
 RC STRAIN-F-9;
 RX MEDLINE=93214115; Pubmed=7763496;
 RA Sakka K., Kojima Y., Kondo T., Karita S.-I., Ohmura K., Shimada K.;
 RT "Nucleotide sequence of the Clostridium stercorarium xynA gene
 encoding xylanase A: identification of catalytic and cellulose
 binding domains";
 RL Biosci. Biotechnol. Biochem. 57:273-277(1993).
 RN [2]
 RP REVISIONS.
 RC STRAIN-F-9;
 RA Sakka K.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- MISCELLANEOUS: HAS THERMOPHILIC PROPERTY (MAXIMUM ACTIVITY AT 70
 DEGREE CELSIUS).
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 HYDROLASES).
 CC -1- SIMILARITY: CONTAINS 2 XYNZ-TYPE CELLULOSE-BINDING DOMAINS (CBD).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC or send an email to license@isb-sib.ch.
 CC EMBL; D13325; BAA02584.1; -
 DR HSSP; P09850; 1XNB.
 DR InterPro; IPR005084; CBM_6.
 DR InterPro; IPR001137; GH_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR Pfam; PF03422; CBM_6; 2.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.
 KW Cellulose degradation; Xylan degradation; Hydrolase; Glycosidase;
 KM Signal; Repeat.
 FT SIGNAL 1 30
 FT CHAIN 31 512
 FT DOMAIN 236 365
 FT DOMAIN 416 504
 FT DOMAIN 124 124
 FT ACT_SITE 215 215
 FT ACT_SITE 236 244
 FT DOMAIN 279 477
 FT DOMAIN 279 340
 FT REPEAT 279 340
 FT REPEAT 416 477
 FT REPEAT 416 477
 FT REPEAT 416 477
 SQ SEQUENCE 512 AA; 55843 MW; 1E133CBF4C139305 CRC64;
 Query Match 42.9%; Score 448.8; DB 1; Length 512;
 Best Local Similarity 46.2%; Pred. No 1.4e-12;
 Matches 90; Conservative 24; Mismatches 59; Indels 22; Gaps 5;
 QY 7 TGYNNGYFYSYWNDHGCVTYTNGPGQFVSVMNSNGNFVGKNGKQPGTKNK----- 58
 DB 39 TGYHGGYDYELMKD-YGNTIMELNDGTFSCOMSNIGNALFRKG-----RKFNSDKTYQ 91
 QY 59 -----VINFSGYNPNNGSYLSYVGMNRNPLEIYIVNEFGTYNPGTATKLGVTSGSYDYI 112
 DB 92 ELGDIIVETGCDNPNNGSYLSYVGMNRNPLEIYIVNEFGTYNPGTATKLGVTSGSYDYI 150
 QY 113 SVYDIIRTONOPSTIGATFYQYVSVRRNRSSGVSNTANHFNMAOQGLTGMDYQ 172
 DB 151 GYVEIYETRVNQPSTIGATFYQYVSVRRNRSSGVSNTANHFNMAOQGLTGMDYQ 210
 QY 173 YAVESYFSSGSASI 187
 DB 211 ALTEVGYOSSGYANV 225
 RESULT 21
 XYNL_TRIRE
 ID XYNL_TRIRE STANDARD; PRT; 229 AA.
 AC P36218;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
 GN XYNL.
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Hypocreaceae; Hypocrea.
 OX NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-QM9414 / Rut C-30;
 RX MEDLINE=93103679; Pubmed=1369024;
 RA Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,
 RA Harkki A., Kubicek C.P.;
 RT "The two major xylanases from Trichoderma reesei: characterization of
 both enzymes and genes";
 RL Biotechnology 10:1461-1465(1992).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=95127663; Pubmed=7827044;
 RA Toerrien A., Rouvinen J.;


```

CC -1- FUNCTION: HAS A LOW PH OPTIMUM (3.0).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: A19535; CA01470.1; -
DR PDB: 1URK; 24-DEC-97.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 1 28
FT ACT_SITE 106 211
FT ACT_SITE 106 106
FT ACT_SITE 197 197
FT DISULFID 119 138
FT PROTON_DONOR.
SQ SEQUENCE 211 AA; 22641 MW; 82BBEBE12ED79303 CRC64;

Query Match 41.5%; Score 434; DB 1; Length 211;
Best Local Similarity 47.3%; Pred. No. 1.2e-12;
Matches 89; Conservative 27; Mismatches 62; Indels 10; Gaps 5;

OY 6 GTGYNNGYFYSYWNDHGCVTYTNGPGQGFVSNMNS--SGNFVGGKGMPGTRKNVYNS 63
DB 30 GINYYQNT-----NGLDGFYTDSE-AGTFSMYWDGVSDDPVYGLGTTGSS-SKATYIS 82
OY 64 GSYNPNNG-NSYLSYVYGMSHNPLEYIYVENFGTYPNSGATKLGKGVTSDDGSVYDIYRQR 122
DB 83 AEYSASGSSSYLAVYGVWNYVPOAEYIYVEDYGDYPCSSATSLGTYVSDGSTYYOCTDTR 142
OY 123 VNOPSITGATFYQYVSVYRNHRSSGSVNTANHFMAQAQGLTGLTMDYQIYAVAGCYSS 182
DB 143 TNEPSITGISTFTQYFVSRESTRISGTYVANHFMFAHFGNSDFNYQVAVVAVMSGA 202
OY 183 GSASITVS 190
DB 203 GSASVTIS 210

RESULT 24
XYN1_ASPTU STANDARD: PRT: 211 AA.
AC P53331; 012568;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYN1 OR XLNA
OS Aspergillus tubingensis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OC NCBI_TaxID=5068;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=NM756;
RA MEDLINE=94344036; PubMed=8065265;
RA de Graaf L.H., van den Broeck H.C., van Ooijen A.J.J., Visser J.;
RT "Regulation of the xylanase-encoding xlna gene of Aspergillus
RL tubingensis.";
RL Mol. Microbiol. 12:479-490(1994).

```

```

RN [2]
RP REVISIONS.
RA de Graaf L.H., van den Broeck H.C., van Ooijen A.J.J., Visser J.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: L26988; AAB05996.1; -
DR HSP: P55329; 1URK.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 27
FT CHAIN 1 28
FT ACT_SITE 106 211
FT ACT_SITE 106 106
FT ACT_SITE 197 197
FT PROTON_DONOR (BY SIMILARITY).
SQ SEQUENCE 211 AA; 22576 MW; 1A88D06C67080D4 CRC64;

Query Match 41.3%; Score 432; DB 1; Length 211;
Best Local Similarity 47.3%; Pred. No. 1.5e-12;
Matches 89; Conservative 25; Mismatches 64; Indels 10; Gaps 5;

OY 6 GTGYNNGYFYSYWNDHGCVTYTNGPGQGFVSNMNS--SGNFVGGKGMPGTRKNVYNS 63
DB 30 GINYYQNT-----NGLDGFYTDSE-AGTFSMYWDGVSDDPVYGLGTTGSSN-ALITYS 82
OY 64 GSYNPNNG-NSYLSYVYGMSHNPLEYIYVENFGTYPNSGATKLGKGVTSDDGSVYDIYRQR 122
DB 83 AEYSASGSSSYLAVYGVWNYVPOAEYIYVEDYGDYPCSSATSLGTYVSDGSTYYOCTDTR 142
OY 123 VNOPSITGATFYQYVSVYRNHRSSGSVNTANHFMAQAQGLTGLTMDYQIYAVAGCYSS 182
DB 143 TNEPSITGISTFTQYFVSRESTRISGTYVANHFMFAHFGNSDFNYQVAVVAVMSGA 202
OY 183 GSASITVS 190
DB 203 GSASVTIS 210

RESULT 25
XYN3_ASPAK STANDARD: PRT: 211 AA.
AC P33557;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 3 precursor (EC 3.2.1.8) (Xylanase 3)
DE (1,4-beta-D-xylan xylanohydrolase 3) (Xylanase C).
GN XYN3
OS Aspergillus awamori (var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OC NCBI_TaxID=40384;
OX [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 28-34.
RC STRAIN=IFO 4308;
RA MEDLINE=93005082; PubMed=1368843;
RA Ito K., Iwashita K., Iwano K.;
RT "Cloning and sequencing of the xynC gene encoding acid xylanase of

```

RT Aspergillus kawachii.":
RL Biosci. Biotechnol. Biochem. 56:1338-1340(1992).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 29-210.
RC STRAIN-IFO 4308;
RX MEDLINE-99127851; PubMed-9930661;
RA Fushinobu S., Ito K., Kono M., Wakagi T., Matsuzawa H.;
RT "Crystallographic and mutational analyses of an extremely acidophilic
RT and acid-stable xylanase: biased distribution of acidic residues and
RT importance of Asp-37 for catalysis at low pH."
RL Protein Eng. 11:1121-1128(1998).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: S45138; AAC60542.1; -
DR EMBL: D14848; BAA03576.1; -
DR PIR: JCI198; JCI198.
DR PDB: 1BK1; 26-MAR-99.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PRO0911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation: Hydrolase; Glycosidase; Signal; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 211 ENDO-1,4-BETA-XYLANASE 3.
FT ACT_SITE 106 106 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 197 197 PROTON DONOR.
FT DISULFID 119 138
SQ SEQUENCE 211 AA; 22560 MW; 68BFE9A0EBFFCC CRC64;

Query Match 41.2%; Score 430.9; DB 1; Length 211;
Best Local Similarity 44.0%; Pred. No. 1.6e-12;
Matches 88; Conservative 28; Mismatches 53; Indels 31; Gaps 6;

QY 21 GH-----GGVYTT--NG-----PGGQFSVMSN--SGNFVGGKQW 51
DB 12 GHAFAPVPQPYLVSRSAGINVQNYNGNLADFTYDESAGFSSMYWEDGVSDFYVGLGW 71
QY 52 OPGTKNKYINFGSGYNPNPG-NSYLSYVGSRNPDIIEYIVENFGTYNPGTKIAGEVTS 110
DB 72 TTGSSN-AISYSAEYASGSSSYLAIVGWVNPQAEYIVEDYGDYVPCSSATSLGTAYS 130
QY 111 DGSVVDIYRTQRPVNPSTIGTATFYQYWSVRNRHSSGSVNTANFNMAOQGLTGTM 170
DB 131 DGSYVQCTDRTNRPSTIGTISTFTQYFSVRSRTSTSGTVYANFNMAOQGFNSDEN 190
QY 171 YQIVAVEGYFSSGASITVS 190
DB 191 YQVMAVEAMSGASASVITIS 210

RESULT 26
XNNA_RUMFL
ID XNNA_RUMFL STANDARD: PRT; 954 AA.
AC P29126;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bifunctional endo-1,4-beta-xylanase Xyla precursor (EC 3.2.1.8).
GN XNNA.

OS Ruminococcus flavefaciens.
OC Bacteria: Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
OC Ruminococcus.
OX NCBI_Taxid=1265;
RN NCBI_Taxid=1265;
RP SEQUENCE FROM N.A.
RX STRAIN-17;
RC MEDLINE-9226318; PubMed-1584021;
RA Zhang J.-X., Flint H.J.;
RT "A bifunctional xylanase encoded by the xyna gene of the rumen
RT cellulolytic bacterium Ruminococcus flavefaciens 17 comprises two
RT dissimilar domains linked by an asparagine/glutamine-rich sequence."
RL Mol. Microbiol. 6:1013-1023(1992).
CC -1- FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYLO-OLIGOSACCHARIDES
CC AND DOMAIN 2 MORE XYLOSE.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
CC G (FAMILY 11 OF GLYCOSYL HYDROLASES).
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
CC F (FAMILY 10 OF GLYCOSYL HYDROLASES).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: Z11127; CAA77476.1; -
DR PIR: S18043; S18043.
DR PIR: S20907; S20907.
DR HSSP: P48793; 1XND.
DR InterPro: IPR001137; GH_11.
DR InterPro: IPR001000; Glyco_hydro_10.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PRO0134; GLHYDRLASE10.
DR PRINTS: PRO0911; GLHYDRLASE11.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation: Hydrolase; Glycosidase; Multifunctional enzyme;
Repeat; Signal.
FT SIGNAL 1 27
FT CHAIN 28 954 OR 28, OR 29 (POTENTIAL).
FT DOMAIN 28 244 BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA.
FT DOMAIN 245 622 XYLANASE DOMAIN 1.
FT DOMAIN 623 954 ASN/GLN/TRP-RICH (LINKER).
FT ACT_SITE 122 122 XYLANASE DOMAIN 2.
FT ACT_SITE 223 223 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 774 774 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 884 884 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 954 AA; 111362 MW; 1033567D4B56EBD CRC64;

Query Match 39.2%; Score 410; DB 1; Length 954;
Best Local Similarity 41.4%; Pred. No. 2.1e-10;
Matches 84; Conservative 33; Mismatches 66; Indels 20; Gaps 6;

QY 4 OPGTGNNGYFYSYVNDGHHGVYTYNGSGQFSVMSNSGPNVG--GKGMPGRTNK--- 58
DB 32 OOTRGNVGGYDEEMNNGQOCASNNPGASFTCSMSINTEFNLMRGNVYSOKKNYAF 91
QY 59 ---VINFSGSYNPNGNSYLSYVGSRNPDIIEYIVENFGTYNP--STGATRLGEVTS DGS 113
DB 92 GNIVLTVDVEYETPRGNSYMCYGVWRNPLMEYIVIEGGMDRPPNDQDEYK-GTVSANGN 150
QY 114 YVDIYRTQRPVNPSTIGTATFYQYWSVRNRHSS-----GSVNTANFNMAOQGLT 165
DB 151 TYDIKRTKRYNPQSLDGTATFPQYWSVRSVOTSGSANNQNTNMYKGTIDVYKHPDAWSAAGLD 210

OY 166 LGTMDYQI-VAVEGYFSSGAS1 187
Db 211 MSGTLYEVSINTEGYRSGSANV 233

RESULT 27

ID	XYND_ROMFL	STANDARD:	PRT:	802 AA.
AC	053317;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Xylanase/beta-glucanase precursor [includes: Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase); Endo-beta-1,3-1,4 glucanase (EC 3.2.1.73) (1,3-1,4-beta-D-glucan-4-glucanohydrolase) (Lichenase)].			
GN	XYND.			
OS	Ruminococcus flavefaciens.			
OC	Bacteris; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;			
OX	Ruminococcus.			
OX	NCBI_Taxid=1265;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN-17;			
RX	MEDLINE-93259938; PubMed-8491715;			
RA	Flint H.J., Martin J., McPherson C.A., Daniel A.S., Zhang J.-X.;			
RT	A bifunctional enzyme, with separate xylanase and beta(1,3-1,4)-			
RT	glucanase domains, encoded by the xynD gene of Ruminococcus			
RT	flavefaciens.";			
RU	J. Bacteriol. 175:2943-2951(1993).			
CC	-1- FUNCTION: CONTAINS TWO CATALYTIC DOMAINS WITH XYLANASE AND ENDO-			
CC	BETA-1,3-1,4 GLUCANASE ACTIVITIES.			
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic			
CC	linkages in xylans.			
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages			
CC	in beta-D-glucans containing 1,3- and 1,4-bonds.			
CC	-1- PATHWAY: Xylan degradation.			
CC	-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULOSE FAMILY			
CC	G (FAMILY 11 OF GLYCOSYL HYDROLASES).			
CC	-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 16 OF			
CC	GLYCOSYL HYDROLASES.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch)			
CC	-----			
DR	EMBL: S61204; AAB26620.1; -			
DR	HSP: P23904; IAK.			
DR	InterPro: IPR003305; CBM_Cenc.			
DR	InterPro: IPR001137; GH_11.			
DR	InterPro: IPR000757; Glyco_hydro_16.			
DR	Pfam: PF00457; Glyco_hydro_11; 1.			
DR	Pfam: PF00722; Glyco_hydro_16; 1.			
DR	Pfam: PF02018; CBM_4_9; 1.			
DR	PRINTS: PR00911; GLHYDRLASE11.			
DR	PRINTS: PS00776; GLYCOSYL_HYDROL_F11_1; 1.			
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
DR	PROSITE: PS01034; GLYCOSYL_HYDROL_F16; 1.			
KW	Xylan degradation; Hydrolase; Glycosidase; Signal;			
KW	Multifunctional enzyme.			
FT	SIGNAL	1	31	POTENTIAL.
FT	CHAIN	32	802	XYLANASE/BETA-GLUCANASE.
FT	DOMAIN	32	244	A (XYLANASE).
FT	DOMAIN	245	523	B.
FT	DOMAIN	524	555	LINKER.
FT	DOMAIN	556	802	C (BETA-GLUCANASE).
FT	ACT_SITE	124	124	NUCLEOPHILE (BY SIMILARITY).
FT	ACT_SITE	226	226	PROTON DONOR (BY SIMILARITY).
FT	ACT_SITE	684	684	NUCLEOPHILE (BY SIMILARITY).

FT DOMAIN 524 529 POLY-THR.
FT DOMAIN 532 543 POLY-THR.
FT DOMAIN 546 553 POLY-THR.
SQ SEQUENCE 802 AA; 89091 MW; 2880A689647284AF CRC64;

Query Match 37.6%; Score 392.5; DB 1; Length 802;
Best Local Similarity 39.4%; Pred. No. 9, 1e-10;
Matches 80; Conservative 31; Mismatches 67; Indels 25; Gaps 6;

OY 7 TGVNNGYFYVNDHGCVTTNGPGCGSVVMSNSGNVGV--GKMGDPGTNRK----- 58
Db 37 TCKVGGFDEWEMNQNTGTVSNMPGAGSFTCSMGIENLARMGRNYDDOKRYAFGDI 96
OY 59 VNFSGSYVNPNSLYVGMGRNPLIEYIYENFGTYNP--STGATKLGEVTSFGSYVD 116
Db 97 VLTIVDEYTPRGNSITNCICGTGRNPLMEYIYEGMGDWPDPDGDVDFGTTIDGKTYK 156
OY 117 IYRTQVRVNPSTIIGATFYQVYSVRNRHSSGS-----VNTANHFVMAAQGLT 165
Db 157 IRKSMRYNPSTIEGRTFPQYWSVR--TSGSRNNTNYMKDQVSVTRKHFDMASKAGLD 213

OY 166 LGTMDYQI-VAVEGYFSSGAS1 187
Db 214 MSGTLYEVSINTEGYRSGSANV 236

RESULT 28

ID	XYNA_NEOPA	STANDARD:	PRT:	607 AA.
AC	P29127;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Bifunctional endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (XYLA).			
GN	XYNA.			
OS	Neocallimastix patriciarum (Rumen fungus).			
OC	Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;			
OC	Neocallimasticales; Neocallimastix.			
OX	NCBI_Taxid=4758;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-93023632; PubMed-1406248;			
RA	Gilbert H.O., Hazlewood G.P., Laurie J.I., Orpin C.G., Xue G.P.;			
RT	"Homologous catalytic domains in a rumen fungal xylanase: evidence			
RT	for gene duplication and prokaryotic origin.";			
RT	Mol. Microbiol. 6:2065-2072(1992).			
CC	-1- FUNCTION: HYDROLYSES XYLANS INTO XYLOBOSE AND XYLOSE.			
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic			
CC	linkages in xylans.			
CC	-1- PATHWAY: Xylan degradation.			
CC	-1- SIMILARITY: THE 43 AA REPEATS ARE SIMILAR TO THOSE IN PIROMYCES			
CC	SP. XYNA, MANA, MANB AND MANC.			
CC	-1- SIMILARITY: THE N-TERMINAL AND C-TERMINAL PARTS BELONG TO			
CC	CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch)			
CC	-----			
DR	EMBL: X65526; CAA46498.1; -			
DR	PIR: S21392; S21392.			
DR	HSP: P33557; IBA1.			
DR	InterPro: IPR002883; CBD_5.			
DR	InterPro: IPR001137; GH_11.			
DR	Pfam: PF00457; Glyco_hydro_11; 2.			
DR	Pfam: PF02013; CBM_10; 2.			
DR	PRINTS: PR00911; GLHYDRLASE11.			
DR	PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 2.			
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 2.			


```

CC IN BINDING THE CELLULASE-HEMICELLULOSE COMPLEX.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- DOMAIN: CONSISTS OF AN N- AND C-TERMINAL CATALYTIC DOMAINS LINKED
CC TO A MIDDLE REITERATED DOMAIN. ONLY THE C-TERMINAL CATALYTIC
CC DOMAIN IS ACTIVE.
CC -1- SIMILARITY: THE 42 AA REPEATS ARE SIMILAR TO THOSE IN MANA, MANB
CC AND MANC; AND TO THOSE OF N.PATRICIARUM XYNA.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X91858; CAA62969.1; -.
DR HSSP: P09850; 1XNB.
DR InterPro: IPR002883; CBD_5.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 2.
DR Pfam: PF02013; CBM_10; 2.
DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; FALSE_NEG.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; FALSE_NEG.
DR KMW: xylan degradation; Hydrolase; Glycosidase; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 625
FT DOMAIN 20 354
FT DOMAIN 255 279
FT DOMAIN 259 278
FT REPEAT 259 268
FT REPEAT 269 278
FT DOMAIN 284 372
FT REPEAT 284 325
FT REPEAT 331 372
FT DOMAIN 374 403
FT DOMAIN 404 625
FT ACT_SITE 510
FT ACT_SITE 603
FT SEQUENCE 635 AA; 68049 MW; 9DA95B6A17290922 CRC64;
Query Match 25.6%; Score 267.3; DB 1; Length 625;
Best Local Similarity 26.2%; Pred. No. 0.00017;
Matches 62; Conservative 41; Mismatches 67; Indels 67; Gaps 10;
OY 4 OPGTGYNN-----GYFSYWN-D-GHGVTYTNRP 31
DB 388 QPTGQSNNSSTNTNFCSTKSHGQSYETSNKVGSIIGVGEIMADSGNNSATFYS-- 445
OY 32 GQFSVNMNSGNEFVGKGMQPGTKNKVYNFSG--SYNPN-----S 72
DB 446 DGSFSCSRNAKDLCSG-----LSFDSTKTYOOLGHMYADEFLVKONTQNDYS 496
OY 73 YLSVYGSRNPLIEYIYENF-GTYNPS--TGATKLEVTSDGSVYDIYRTQRYNPSII 129
DB 497 YVGIGYTRNPLVEFYVDMNLSQMRPGDWGKNNKHDFITDGAKYTYEYENTRIG-PSID 555
OY 130 GTATFYQWYVRNRHSSGSVNTANHNMAOGLTLGTM-DYOIVAVEGYFSSGSA 185
DB 556 GNTTFKQYFISROARDCGITIDITAHFEQWEKLCMRGKMEAKVLCBAGSTSGSTS 612

```

```

DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Muramidase-2 precursor (EC 3.2.1.17) (1,4-beta-N-
DE acetylmuramoylhydrolase) (peptidoglycan hydrolase) (Pg-hydrolase-2)
DE (Lysosome).
OS Enterococcus hirae.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxId=1354;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-73.
RC STRAIN=ATCC 9790;
RX MEDLINE=92165737; PubMed=1347040;
RA Chu C.-P., Kariyama R., Daneo-Moore L., Shockman G.D.;
RT "Cloning and sequence analysis of the muramidase-2 gene from
RL Enterococcus hirae."
RN J. Bacteriol. 174:1619-1625(1992).
RP [2]
RP FUNCTION.
RC STRAIN=ATCC 9790;
RX MEDLINE=89327152; PubMed=2753858;
RA Dollinger D.L., Daneo-Moore L., Shockman G.D.;
RT "The second peptidoglycan hydrolase of Streptococcus faecium ATCC 9790
RL covalently binds penicillin."
RN J. Bacteriol. 171:4355-4361(1989).
RP [3]
RP FUNCTION.
RC STRAIN=ATCC 9790;
RA Del Mar Lleo M., Canepari P., Satta G.;
RT "Thermosensitive cell growth mutants of Enterococcus hirae that
RL elongate at non-permissive temperature are stimulated to divide by
RP parental autolytic enzymes."
RN J. Gen. Microbiol. 139:3099-3117(1993).
CC -1- FUNCTION: MAY WORK IN CONCERT WITH AND POTENTIATE THE PROCESSIVE
CC HYDROLYTIC ACTION OF MURAMIDASE-1, WHICH REQUIRES BINDING OF THE
CC ENZYME TO NONREDUCING ENDS OF GLYCAN CHAINS. HYDROLYSIS IN THE
CC MIDST OF GLYCAN CHAINS WOULD INCREASE THE NUMBER OF BINDING SITES
CC FOR MURAMIDASE-1. MAY FUNCTION IN FACILITATING SEPTUM FORMATION
CC AND CELL SEPARATION. ACTIVE ON M. LOREUS CELL WALLS AND ON E. HIRAE
CC CELL WALL FRACTIONS. BUT NOT ACTIVE ON E. HIRAE INTACT CELL WALLS.
CC CAN COVALENTLY BIND PENICILLIN.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
CC acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
CC heteropolymers of the prokaryotes cell walls.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN
CC BINDING.
CC -1- SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
CC -1- SIMILARITY: CONTAINS 6 LYSM REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M77639; AAA24776.1; -.
DR PIR: A42296; A42296.
DR HSSP: P22629; 1SMD.
DR InterPro: IPR002901; Amidase_4.
DR InterPro: IPR002482; LYSM.
DR Pfam: PF01476; LysM; 6.
DR Pfam: PF01832; Amidase_4; 1.
DR SMART: SM00047; Lys2; 1.
DR SMART: SM00257; LysM; 6.
KW Hydrolase; Glycosidase; Bacteriolytic enzyme; Cell wall;
KW Cell division; Septation; Repeat; Signal.
FT SIGNAL 1 49
FT CHAIN 50 666
FT REPEAT 257 299
FT REPEAT 338 380
FT REPEAT 414 456

```

```

RESULT 31
MUR2_ENTNR STANDARD; PRT; 666 AA.
ID MUR2_ENTNR
AC P39046;
DT 01-FEB-1995 (Rel. 31, Created)

```



```

FT REPEAT 489 531 LYSM 4.
FT REPEAT 565 607 LYSM 5.
FT REPEAT 623 665 LYSM 6.
SQ SEQUENCE 666 AA: 70670 MW: FFOA/FAFCDB10BA3 CRC64:

Query Match 15.7%; Score 163.6; DB 1; Length 666;
Best Local Similarity 17.5%; Pred. No. 6.4;
Matches 70; Conservative 28; Mismatches 68; Indels 234; Gaps 16;

OY 7 TGYNCEYS-YW-----N 19
DB 161 TFSFGVYYAGTWKSNKSYDTACTLGRYATPDGYAGKLNIIITTYGLTKYDPASGN 220
OY 20 DSHGCVTYTNGPG-GQFSYVMSNSGNFYVGKGMQPT----- 55
DB 221 AG-GGVTTINGNGTGTGNTSGTSGN-SGGSATTCTTYYKSGDSVNGISHFGITMAQ 278
OY 56 -----KKKVI-----NFGSYNPGNS----- 72
DB 279 LIEWNNIKNNFYPGOKLTIKGQASSTTNTGNASSGNTSGNTSGTGOATGAKY 338
OY 73 -----YLSVGMNRNPLEYIYVENFTY-----NPSTGAT 103
DB 339 TVKSGDSVWKIANDHISMOLIEWNNIKNNFYPGQOLVSKGSSSAGSTISNTSTGNT 398
OY 104 -----KLGEVTSQDSYDIYRTQRYVQPSITIGTATFYQWYVR----- 142
DB 399 SSSNTANTGSTTS-GSYTYVKAGESV-----WSVSNKFCISMNOLIQWNNIK 443
OY 143 -----NHRSSGYNVTANHN-----AMA--Q 161
DB 444 NNFTYPGOKLIVKGGSSSNASTSTANNKNTASSNTSTATGQATYTVKAGESWGVANK 503
OY 162 OGILTLGTM-----DYOIVAVEGFSSGSASTIV 189
DB 504 NGISMOLIEWNNIKNNFYPGOKLIVKGGSSKASATPATI 543

RESULT 32
ISOA_PSEAV
ID ISOA_PSEAV STANDARD: PRT: 776 AA.
AC P10342;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Isoamylase precursor (EC 3.2.1.68).
GN IAM.
OS Pseudomonas amyloclaterosa.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=32043;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN=SB-15;
RX MEDLINE=88243808; PubMed=3379068;
RA Amenura A., Chakraborty R., Fujita M., Nouni T., Futai M.;
RT "Cloning and nucleotide sequence of the isoamylase gene from
RT Pseudomonas amyloclaterosa SB-15.";
RL J. Biol. Chem. 263:9271-9275(1988).
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN=JD210;
RX MEDLINE=91064385; PubMed=2248978;
RA Chen J.H., Chen Z.Y., Chow T.Y., Chen J.C., Tan S.T., Hsu W.H.;
RT "Nucleotide sequence and expression of the isoamylase gene from an
RT isoamylase-hyperproducing mutant, Pseudomonas amyloclaterosa JD210.";
RL Biochim. Biophys. Acta 1087:309-315(1990).
RN 13;
RP SEQUENCE OF 744-776 FROM N.A.
RC STRAIN=SB-15;
RX MEDLINE=89327147; PubMed=2753857;
RA Amenura A., Fujita M., Futai M.;
RT "Transcription of the isoamylase gene (iam) in Pseudomonas
RT amyloclaterosa SB-15.";

```

```

RL J. Bacteriol. 171:4320-4325(1989).
[4]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=98387895; PubMed=9719642;
RA Katsuya Y., Mezaki Y., Kubota M., Matsuura Y.;
RT "Three-dimensional structure of Pseudomonas isoamylase at 2.2-A
RT resolution.";
RL J. Mol. Biol. 281:885-897(1998).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(1,6)-D-glucosidic branch
CC -1- Linkages in glycogen, amylopectin and their beta-limit dextrins.
CC -1- INDUCTION: BY MALTOSE.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY, ISOAMYLASE SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: J03871; AAA25854.1; -
DR EMBL: X13378; CAA31754.1; -
DR PIR: A28109; A28109.
DR PDB: 1BR2; 12-AUG-98.
DR InterPro: IPR000461; Alpha-amylase.
DR InterPro: IPR004193; Isoamylase-N.
DR Pfam: PF00128; alpha-amylase-N.
DR Pfam: PF02922; isoamylase-N; 1.
KW Hydrolyase; Glycosidase; signal; 3D-structure.
FT SIGNAL 1 26
FT CHAIN 27 776
FT ACT_SITE 401 401
FT ACT_SITE 481 481
FT ACT_SITE 536 536
FT DISULFID 410 422
FT DISULFID 546 616
FT DISULFID 738 766
FT CONFLICT 8 8
FT CONFLICT 126 126
FT CONFLICT 169 171
FT CONFLICT 386 386
FT CONFLICT 413 416
FT CONFLICT 454 489
FT
FT CONFLICT 555 556
FT CONFLICT 650 657
FT SEQUENCE 776 AA: 83626 MW: F738BF8040246169 CRC64;

Query Match 14.9%; Score 155.3; DB 1; Length 776;
Best Local Similarity 10.9%; Pred. No. 20;
Matches 74; Conservative 26; Mismatches 60; Indels 517; Gaps 18;

OY 13 YFYSYNNDDHG--GVTYNGPCGQ-----FVWWSMS 42
DB 59 YLKS---AGYVOESATITLSPAGSGVMATVVSIIKAIGTGANVYGYGRAMGPWWPYA 115
OY 43 GNEFGKGMQPG-----TRNKVI----- 60
DB 116 SNW--GKGSQAGFVSDVANDGNDRFNPKNLLDPYAEQVSODPLNPSNONGNVFASGASYR 173
OY 61 -NNGSYNNG----- 70
DB 174 TTDGSLYAPKGVVLPSTOSTGTPTRAKQDDVIEVHVGFTEDTSLPAQYRGTYGA 233
OY 71 ---NSYL----- 74
DB 234 GLKASTLASIGYTAVEFLVQETQNDANDVVPASDANQNTGMYTENSPPDRRYANKA 293
OY 75 -----SVYGMNRNPLEYI- 88

```

Db 294 AGGPTAEFQAMQAFHNAIGKYYMDVYVYNTAEGTWTSSDPTTATYISMRGLDNATYFE 353
QY 89 -----IVENFGTYN----- 97
Db 354 LTSGNOYFYDNTGIGANFNFTYNTVAQNLIVDSLAVYANTMGVDFRDLASVLGNSCLNG 413
QY 98 -----PSTGAT----- 103
Db 414 AYTAAPNCNPGYNFDAADSNVAINRLREFYVRAAGSGGLDLFAEPAWAGNSYQLG 473
QY 104 -----KLGFTSDGSYVDIYRTORVNO----- 125
Db 474 GFPQGSSEWNGLEFRDLRQANLGSMT-----IYVTDADNDFSGSSNLFOSSGRSPW 526
QY 126 -----PSIIGTATFYQY----- 137
Db 527 NSINFIDVHDMTLKDVYSCNGANNSQAMPYGPSDGTSTNYSDQMSAGTGAADVQRR 586
QY 138 -----MSV----- 140
Db 587 AARTGMAFEMLSAGTPLMGSGDEYLRTLCNNNAVNLDSANMLTYSMTTDSNFTFAQ 646
QY 141 -----RRNH-----RSSGSV-----NTANHFNAQAQGLTLGTMVY 171
Db 647 RLIAFRKRAHPLRPSSWYSSQLTWYQPSGAVADSNVWNTSNVATAYAINGPSLSDSNS 706
QY 172 QIVAVEGFFSSGSASIT 188
Db 707 IYVAYNGW-----SSSVT 719

RESULT 33
ID ISOA_PSESP STANDARD: PRT: 776 AA.

AC P26501:
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Isoamylase precursor (EC 3.2.1.68).
GN IAM.
OS Pseudomonas sp. (strain SMP1).
OC Bacteria: Proteobacteria.
OX NCBI_TaxID:306;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 27-44.
RX MEDLINE=89381677; PubMed=2778432;
RA Tognoni A., Carrera P., Galli G., Lucchese G., Camerini B.,
Grandi G.,
RT Cloning and nucleotide sequence of the isoamylase gene from a strain
of Pseudomonas sp.
RL J. Gen. Microbiol. 135:37-45(1989).
CC CATALYTIC ACTIVITY: Hydrolysis of alpha-(1,6)-D-glucosidic branch
linkages in glycogen, amylopectin and their beta-limits dextrans.
CC INDUCTION: BY MALTOSE.
CC SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY, ISOAMYLASE SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC -----
EMBL: M25247; AAA25855.1;
DR EMBL: A10909; CA000929.1;
DR PIR: A37035; A37035.
DR HSSP: P10342; 1BF2.
DR InterPro: IPR000461; Alpha_Amylase.
DR InterPro: IPR004193; Isoamylase_N.
DR Pfam: PF00128; Alpha_Amylase; 1.
DR Pfam: PF02922; Isoamylase_N; 1.

KW Hydrolyase; Glycosidase; signal.
FT SIGNAL 1 26
FT CHAIN 27 776 ISOAMYLASE
FT ACT_SITE 401 401 BY SIMILARITY.
FT ACT_SITE 481 481 BY SIMILARITY.
FT ACT_SITE 536 536 BY SIMILARITY.
FT ACT_SITE 546 546 BY SIMILARITY.
FT DISULFID 410 422 BY SIMILARITY.
FT DISULFID 546 616 BY SIMILARITY.
FT DISULFID 738 766 BY SIMILARITY.
SO SEQUENCE 776 AA; 83656 MM; A5B4C02EF026A3A4 CRC64;

Query Match 14.9%; Score 155.3; DB 1; Length 776;
Best Local Similarity 10.9%; Pred. No. 20;
Matches 74; Conservative 26; Mismatches 60; Indels 517; Gaps 18;

QY 13 YFYSYNDHG---GYTYTNGPGQ-----FSYKMSNS 42
Db 59 YLYS--AGYVESATYTLSPAGSGVMAVTPVSSIKAGITGAVYGYRANGPMVPA 115
QY 43 GNFFVGKGMOPG-----TKNKVI----- 60
Db 116 SNM--GKSGAGSYSDVANGDRFNPKLLDPRAGEVSODPLNPSNQNGVFAASASR 173
QY 61 -NFGSYNPG----- 70
Db 174 TTDSGIYAPKGVLLVPSTGSGTKPTRAQKDVYEYVHVGFTEDTSPAPYRGTYGA 233
QY 71 ---NSYL----- 74
Db 234 GLKASYLASLGVTAVEFLPVQETQNDANDVYVNSDANQNYWYNTENYFSPDRRYANKA 293
QY 75 -----SVYGSRNPLIEY- 88
Db 294 AGGPTAEFQAMQAFHNAIGKYYMDVYVYNTAEGTWTSSDPTTATYISMRGLDNATYFE 353
QY 89 -----IVENFGTYN----- 97
Db 354 LTSGNOYFYDNTGIGANFNFTYNTVAQNLIVDSLAVYANTMGVDFRDLASVLGNSCLNG 413
QY 98 -----PSTGAT----- 103
Db 414 AYTAAPNCNPGYNFDAADSNVAINRLREFYVRAAGSGGLDLFAEPAWAGNSYQLG 473
QY 104 -----KLGFTSDGSYVDIYRTORVNO----- 125
Db 474 GFPQGSSEWNGLEFRDLRQANLGSMT-----IYVTDADNDFSGSSNLFOSSGRSPW 526
QY 126 -----PSIIGTATFYQY----- 137
Db 527 NSINFIDVHDMTLKDVYSCNGANNSQAMPYGPSDGTSTNYSDQMSAGTGAADVQRR 586
QY 138 -----MSV----- 140
Db 587 AARTGMAFEMLSAGTPLMGSGDEYLRTLCNNNAVNLDSANMLTYSMTTDSNFTFAQ 646
QY 141 -----RRNH-----RSSGSV-----NTANHFNAQAQGLTLGTMVY 171
Db 647 RLIAFRKRAHPLRPSSWYSSQLTWYQPSGAVADSNVWNTSNVATAYAINGPSLSDSNS 706
QY 172 QIVAVEGFFSSGSASIT 188
Db 707 IYVAYNGW-----SSSVT 719

RESULT 34

AMYG_RHIOR
ID AMYG_RHIOR STANDARD: PRT: 604 AA.

AC P07683;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Glucoamylase precursor (EC 3.2.1.3) (Glucon 1,4-alpha-D-glucosidase)
(1,4-alpha-D-glucan glucohydrolase).

QY 139 -----SVRRNRSSGSVNTANHFN-AW----- 159
DB 446 KLKADLPPTGTPVPDPTAPSPGNAIRSTGV--TANSVTLAMNASTDNDVGTGVNYNGA 503
QY 160 -----AAGGLTIGCT-MDYQIVAVE--GYSSSGSASITVS 190
DB 504 NLATSVTGTATATISGLTGTAGTSTYTFRIKAKDAAGNLAAASNAVTVS 548

RESULT 37
BCN5_CLOPE STANDARD: PRT: 890 AA.
AC P08696:
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Bacteriocin BCN5.
CN BCN:
OS Clostridium perfringens.
OG Plasmid pip404.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OX Clostridia.
RN NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CPN50;
RX MEDLINE=88336297; PubMed=2901768;
RA Garner T., Cole S.T.;
RT "Complete nucleotide sequence and genetic organization of the
bacteriocinogenic plasmid, pip404, from Clostridium perfringens.";
RL Plasmid 19:1134-1150(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CPN50;
RX MEDLINE=87057020; PubMed=2877971;
RA Garner T., Cole S.T.;
RT "Characterization of a bacteriocinogenic plasmid from Clostridium
perfringens and molecular genetic analysis of the
bacteriocin-encoding gene.";
RL J. Bacteriol. 168:1189-1196(1986).
RN [3]
RP SEQUENCE OF 1-14 FROM N.A.
RC STRAIN-CPN50;
RX MEDLINE=89039249; PubMed=2460717;
RA Garner T., Cole S.T.;
RT "Studies of UV-inducible promoters from Clostridium perfringens in
vivo and in vitro.";
RL Mol. Microbiol. 2:607-614(1988).
CC -1- INDUCTION: MAY FUNCTION AS AN IONOPHORE.
CC -1- INDUCTION: BY UV IRRADIATION.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M14481; AAA98248.1; -
DR EMBL: M32882; AAA98249.1; -
DR PIR: A30481; A30481.
DR InterPro: IPR003646; SH3_bac.
DR SMART: SM00287; SH3b_3.
KW Antibiotic; Bacteriocin; Plasmid.
FT DOMAIN 815 869 HTDROPHOBIC.
SQ SEQUENCE 890 AA; 96699 MW; F4E5E8971C31C6C6 CRC64;

Query Match 13.8%; Score 143.7; DB 1; Length 890;
Best Local Similarity 14.4%; Pred. No. 81;
Matches 61; Conservative 29; Mismatches 81; Indels 253; Gaps 15;
QY 1 OTIOGC-----TGYNNGYF-----YSYWN----- 19

DB 45 RTVSDGEITVLFTSNEKNIVLVQYPTSSGFGQGVNTATSIIRKKDDYSWNGSTPEPV 104
QY 20 -----DGHGVTYTNPGGQFS---VNMNSGTFNVGCKQM 52
DB 105 YDEPDTTIGTLDPRERAVLVKKYDGMVYVADTGTGKLTNLSGLVHYEGSGSTG 160
QY 53 PGTNRKVINSGSYN-----PNCN----- 71
DB 161 -----GSFNGVAPGEVPPGFTYENNAEYVGDGLYRDANGNLIPGRSVSGDK 209
QY 72 -----SYLSVYGWSRNPLEYIVEN---F 93
DB 210 ITVLDPGYTKOLALVQYPAGDVPRQGYVTNATNLIRFYNOYSMHNGSTSEEVLDENGHL 269
QY 94 GTYNPSTGATKLGVEITSQGSVYDIYRTOR-----VNPSTIGTAT 133
DB 270 GSLNPEYEAATLLYE--KNGMKHVYVDYTNKGPNPTKSGYVKEGAATRVDPDIPPSITNAOK 327
QY 134 FYQYWSVRNRHSSGSVNTANHFNA-----WAQGLTL----- 166
DB 328 I--VYGISGRGRELAAKYVNGNSNLVFCATHGEMDMADGIELTIRGNGLIEHPONA 385
QY 167 GTMDYQIVAV-----EGY-----FSSGSAS 186
DB 386 GTNMNSLVIIPVANDGLSEGTNNPGRCITVCAVDCNRDPEPLGFSPOGVPYRHSGSEP 445
QY 187 ITVS 190
DB 446 LSVS 449

RESULT 38
AMTB_PAPEO STANDARD: PRT: 1196 AA.
ID AMTB_PAPEO
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta/alpha-amylase precursor [includes: Beta-amylase (EC 3.2.1.2);
Alpha-amylase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
active fragments of the Bacillus polymyxa beta-amylase.";
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "A single gene directs synthesis of a precursor protein with beta-
amylase and alpha-amylase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN-ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amylase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;

SO	SEQUENCE	1196 AA:	130893 MM:	A4LEA6B70F257064 CRC64:
QY	Query Match	13.7%	Score 143.5;	DB 1; Length 1196;
Db	Best Local Similarity	10.1%;	Pred. No. 1.4e+02;	
Matches	75;	Conservative	25;	Mismatches 70; Indels 575; Gaps 20;
QY	2	TIQPGCTGVNNCKFY-	-----	SYWNQGH- 22
Db	462	TIYKKGKFNSEPIYHYRPAGSGWTAAPGVKKODAEISGYAKITVDIGASOLEAFAFNDGNN	521	
QY	23	-----	GGVYTTNGPCGQFSEVNMNSGNEFVG--	-KKMQP-----GTAKNKYI-- 60
Db	522	NMDSNNTKKNYSFSGTSTYTPGNSG	-----	NAGTITSGAPAAANGDGGGTTNKYTV 574
QY	61	---NFSG---SYNNGNSYLSVYG-	-----	-----WS 80
Db	575	YKKGFSNPIYHYRPAGSGWTAAPGVKKODAEISGYAKITVDIGASOLEAFAFNDGNNWD	634	
QY	81	RNPLEIYEIVENFGSTYMP-	-----	STGATKIGEVT----- 109
Db	635	SNNTKNTLFSGTSTYTPGNSGAGGTTRTGAPSGSVLSYVSTYATDLNEVTGQIOTEKL	694	
QY	110	-----	-----	----- 109
Db	695	SGVSLNVTSTYAPNSNGVEVTAQTEAPSGAFSTMDLGLTSLNPTSLNTDWSKOSIYEIMT	754	
QY	110	---SDGS-----	-----	----- 113
Db	755	DRENSGDSNDNYGCGFNSNSDQKKHGGDFQGLINKLDYIKNNGFTAIWITPYTMOKSE	814	
QY	114	-----VYDIYRT-----	-----	----- 120
Db	815	YAYHGTYTFEYFVAVDGLGTMDKLOELVRKAHDKNIAMVYVYVHTGDFQPGNGFAKAP	874	
QY	121	-----	-----	----- 120
Db	875	FDRKADWTHHNGDITDGDYNSNMOKIENGDAVAGLDLHNHPATANELKMWIKWLNETG	934	
QY	121	-----	-----	----- 133
Db	935	IDGLRLDTVKHKVPKGLKDFQAAINFPTMGEIFPHGDAVYGDYRILDALDPMYTYIK	994	
QY	134	-----	-----	----- 133
Db	995	DVFGHDQSMRKIKDRYSDDRYRDAQTNGVFIIDNHDKRFLINDASGRGANGYDKMPOLKA	1054	
QY	134	-----	-----	----- 146
Db	1055	ALGFTLTLSRGPIITYOGETEGYSGGDDPAPNRENNFNANNDLYIYIAKLKLVYRNHHPALO	1114	
QY	147	SGS-----	-----	----- 170
Db	1115	NGSOREKMWVDSEFYFORSKNGDEAIVFIN-----	NSMNSQTRIFGNFDNLINSGTRLTNQ	1169
QY	171	-----VOIYAVEGYFSSGSASITVS	190	
Db	1170	LSNDSVOI-----	NNGSTIVTLA	1187
RESULT 39				
FIMD_ECOLI				
ID	FIMD_ECOLI	STANDARD;	PRT;	878 AA.
AC	P30130;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Outer membrane usher protein fimD precursor.			
GN	FIMD OR B4317.			
OS	Escherichia coli.			
CC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
CC	Escherichia.			
OX	NCBI_TaxID=562;			
ON	11			

RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=90220509; PubMed=1970114;
RA Klemm P., Christiansen G.;
RT "The fimD gene required for cell surface localization of Escherichia
RL coli type 1 fimbriae."
RM Mol. Gen. Genet. 220:334-338(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Butland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RB Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RL region from 92.8 through 100 minutes."
RN Nucleic Acids Res. 23:2105-2119(1995).
CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF FIMBRIAL
SUBUNITS ACROSS THE OUTER MEMBRANE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (by similarity).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X11655; CA35968.1; -
DR EMBL; U14003; AAA97213.1; -
DR EMBL; AE000502; AAC7273.1; -
DR PIR; S11886; S11886
DR Ecocore; EGI0311; fimb.
DR InterPro: IPR00015; fimb_usher.
DR Pfam: PF00577; usher.1.
DR PROSITE; PS01151; FIMBRIAL_USHER.1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal;
KW Complete proteome.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 878 OUTER MEMBRANE USHER PROTEIN FIMD.
FT DISULFID 855 877 POTENTIAL.
FT CONFLICT 143 148 QDATAH -> RLTLRT (IN REF. 1).
FT CONFLICT 352 402 DGSFOIFVPSVPLQRECHRYSTAGYRSGNQOEK
TRFOSTLIH -> VIARRELPYPIRFPPLNKAISLFH
YGRRIPESSRKRPAPSRVYSN (IN REF. 1).
FT CONFLICT 658 670 GGDNSSGSTGYAT -> EAMEIAEQATP (IN REF.
1).
FT CONFLICT 723 742 APGARDAKVENOTGVRTDWR -> RLAKQMKGSKTRGAVR
LA (IN REF. 1).
FT FT
SQ SEQUENCE 878 AA; 96482 MW; B2B86CC44FAB7B0F CRC64;
Query Match 13.6%; Score 142.2; DB 1; Length 878;
Best Local Similarity 16.2%; Pred. No. 92;
Matches 51; Conservative 20; Mismatches 46; Indels 198; Gaps 12;
OY 1 OTIOPGTGY-----NNGEYFYSYWNDDHGCVTYTNGPG----- 32
DB 1 : ||| | ||| :
DB 71 QELPPGT-YRVDIYLNNGIMAT-----RDYTFNTGDSGCIIVCLTRIAQLASGLTAS 123
OY 33 -----GQFSVNMNSNGNFVGKG-----WOPGTK 56
DB 124 VAGNNLLADACVPLTTMYQDATAHLADVGQORLNLITPQAFMSNRARCIPELMDPCIN 183
OY 57 NKVTFNGSYNPNGNSLISYGVSRNPLIEYIYENFGTYNPSGATKLGVTSDGSYVD 116
DB 184 AGLLN-----YNFSGS-----VON----- 198
OY 117 IYRTQVNPSTIITAFYQY-----WSVRNRHSSGSVYTNANFN 157
DB 199 -----RIGGSHYALNLOSGLNIGAMRLRDNNTTWSYNSDRSSGSKKKWQHIN 247

OY 158 AMAOOG-----LTLTMDYQIVAVEGY----- 179
DB 248 TWLERDIILPILRSRLTLG-----DSYTGGLDFDGINFRGAQLASDNNMLPDSORGFA 298
OY 180 -----FSSGSASTIV 189
DB 299 PVHIGIARGTAQVVI 313
RESULT 40
VG37_BPT2
ID VG37_BPT2 STANDARD; PRT; 1341 AA.
AC P07067;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Long tail fiber protein p37 (Protein GP37) (Receptor recognizing
DE protein).
GN 37.
OS Bacteriophage T2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10664;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87112716; PubMed=3806672;
RA Riede I., Drexler K., Eschbach M.-L., Henning U.;
RT "DNA sequence of the tail fiber genes 37, encoding the receptor
RL recognizing part of the fiber, of bacteriophages T2 and K3."
RN J. Mol. Biol. 191:255-266(1986).
CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE DISTAL-HALF TAIL FIBER.
CC -1- SUBUNIT: THE DISTAL HALF-FIBER CONTAINS TWO MOLECULES EACH OF GP36
CC AND GP37 AND ONE MOLECULE OF GP35.
CC
CC -1- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X04442; CAA28038.1; -
DR PIR; S09579; S09579.
KW Fiber protein.
SQ SEQUENCE 1341 AA; 143152 MW; 1B7981E7EA5FA7F5 CRC64;
Query Match 13.5%; Score 141.4; DB 1; Length 1341;
Best Local Similarity 11.2%; Pred. No. 2; 2e+02;
Matches 80; Conservative 29; Mismatches 69; Indels 536; Gaps 24;
OY 1 OTIOPGTGYNNGY-----STW-----ND 20
DB 222 QYVYPGCGEENGIMYLKRVRAKSGGTYHEIASAQTKNDEISWWTGTLTKLMGLND 281
OY 21 G----- 21
DB 282 GAVYLRSLAIGTITADENTNNYCSPTIPMGERTIALGDATGLYIKQGYDLVGNNSV 341
OY 22 -----HGGVYTV-----NGPGQFSVNMNS 42
DB 342 ASITPDSFRSTRKALFGSSEGGG-TWTMPETNALLSVQOADVNNAGDQTHIGYNSG 400
OY 43 G---NFGGKG----- 50
DB 401 GKMSHYFRGKQOTINIOKMEVNPGLKLVTDSENNVOFYANGTVSSIORIKPDNGLVLT 460
OY 51 -----WOPGTR-----NK-----VINSGSYNPNG----- 70
DB 461 GAPPDGIQLDAPTAADTKTILMAGGTRAGONKSYVSIKAGNSFNASGRARETVREVG 520
OY 71 -----NSYLSAYVG- 78

```

Db 521 DQGFHFYSQVAPAPAGSTVGPDIOLRVNGLLTAGSIVASGITTESSILNVNGLSVNGO 580
OY 79 -----WS-----RNPLEIYIV-----90
Db 581 AKFGGTANALRTIMNAEYCIFFRSESNTFIITPTNONEGESGDHSLRPVIRIGLNDGAVG 640
OY 91 -----ENF-----93
Db 641 LGRDSEIYDQNNALTTINSNRINANFRMQLGOSTYIDAECTDTPRACAGSFVSQNNEN 700
OY 94 -----GTY-----NPSTGATK 104
Db 701 VRAPYMINRTDTSTVPIIKORYQVQNSCYSLGTLSTGDFRIHYHGGGNGSGTGPOK 760
OY 105 L-----GEVT-----SDGSV 114
Db 761 ADLANOFRRDGSFRSPNKIEINAVITIGTDGNTTGGTGNFANLNTLNKRTTYGVGMASSV 820
OY 115 YDIYTORVNOPSIIGTATFYQYWSVRNRHRSRGSV-----NPNAN 154
Db 821 VGMVFATVITPOSTGTVF-----KISGAGFNFKSYNQASIAEIVLRTGNMFX 870
OY 155 HENA--WAQGL-----TLGTM--YQI-VAVEGYFS-----SGSASTY 189
Db 871 GINAVALMNRSDLSFNQIATMNTSDTYDYVFCGYTALIVEYSCSENSVTV 924

```

RESULT 41

```

SACB_STRSL STANDARD: PRT: 969 AA.
AC 055242:
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Levanucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl
  transferase) (Sucrose 6-fructosyl transferase).
OS Streptococcus salivarius.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
  Streptococcus.
OX NCBI_TaxID=1304;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25975; PubMed=8331080;
RX MEDLINE=93322332; PubMed=8331080;
RA Rathnam C., Giffard P.M., Jacques N.A.;
RT "The cell-bound fructosyltransferase of Streptococcus salivarius: the
  carboxyl terminus specifies attachment in a Streptococcus gordonii
  model system." 175:4520-4527(1993).
RL J. Bacteriol. 175:4520-4527(1993).
CC -1- CATALYTIC ACTIVITY: Sucrose + {(2,6)-beta-D-fructosyl}(N) =
  glucose + {(2,6)-beta-D-fructosyl}(N+1).
CC -1- SUBCELLULAR LOCATION: SECRETED. CELL-WALL BOUND.
CC -1- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC EMBL: L08445; AAA71925.1;
DR InterPro: IPR003469; Glyco_hydro_68.
DR Pfam: PF02435; Glyco_hydro_68; 1.
DR TIGRfams: TIGR01168; YSIRK_signal; 1.
KW Transferrase; Glycosyltransferase; Signal; Cell wall.
FT SIGNAL 1
FT CHAIN 1
FT SEQUENCE 969 AA: 103983 MW: D389B5B32AC735A CRC64:

```

Query Match 13.5%; Score 140.6; DB 1; Length 969;
 Best Local Similarity 17.2%; Pred. No. 1.3e+02;
 Matches 73; Conservative 19; Mismatches 78; Indels 254; Gaps 19;

```

OY 6 GTG-----YNN-----GYF-----14
Db 230 GTGTSILYRNLMKDIVASFLKQDSKLAVPEFKADITIIIMPATVDAQTAKKEIDVWDSW 289
OY 15 -----YSYWN-----GHGVTYTNKPGCGFSVN-- 38
Db 290 PVQDAKSGVYSNMNGYQLYISAGAPNKNSHIYLLRYKYGDNFTHKMKNAGPIFGYNAL 349
OY 39 -----WSNS-----GNFYGK--GMQ-----PGTKKV 59
Db 350 EDDQMGSGATVNSDGSIGLYTYTKNDTSGKLMQGLASATLNLAVENDEVYKSEVDNH 409
OY 60 INFSG-----SY-----NP-----NGNSYL-----74
Db 410 ILFGDNYHYQSYPRFMSFTFDDHNDGNPDRFDNYCLRDPHIIEDNGSRYLIFESNIGD 469
OY 75 -----SYGWSRNPLEIY-----IVENGY-----NPSTGATKGEV 108
Db 470 ENYQGEKQIYKSN-----YGGDAFNLSKFLNLYNNKHLNLSAMANGSIGILKLDON 523
OY 109 TSDGSVYDIYR-----TORVNQPSIIGTATFYQYWSVRNRHRS-----146
Db 524 EKNPSVAVELTYPLVTSNHWTDVEPRSVKMGCKYLLFTASINIKSTDAECTVAAREAVG 583
OY 147 -----SGSVNPNANHNANAQGLTIGTDYQIVAVEGYFSSGS 184
Db 584 DDVVALGFEVSDLSRGKRYPLNGSGVLTASVPADM-----RTSYSYAVPVEG--SSDT 636
OY 185 ASIT 188
Db 637 LLVT 640

```

RESULT 42

```

OM3A_RHILV
ID OM3A_RHILV STANDARD: PRT: 366 AA.
AC 005811:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Outer membrane protein IIIA precursor (OMP111A).
GN ROP.
OS Rhizobium leguminosarum (biovar viciae).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
  Rhizobium.
OX NCBI_TaxID=387;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-31.
RC STRAIN=248;
RX MEDLINE=92104965; PubMed=1370281;
RA de Maagd R.A., Mulders I.H.M., Canter Cremers H.C.J.,
  Lugtenberg B.J.J.;
RT "Cloning, nucleotide sequencing, and expression in Escherichia coli
  of a Rhizobium leguminosarum gene encoding a symbiotically repressed
  outer membrane protein." 174:214-221(1992).
RL J. Bacteriol. 174:214-221(1992).
CC -1- FUNCTION: MAY ACT AS AN OUTER MEMBRANE PORE.
CC -1- SUBUNIT: FORMS CALCIUM-STABILIZED OLIGOMERS.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- DEVELOPMENTAL STAGE: REPRESSED IN THE BACTEROID FORM DURING
  SYMBIOSIS.
CC -1- PTM: ATTACHED COVALENTLY TO PEPTIDOLYCAN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/announce/

```


or send an email to license@lsb-slb.ch).

CC EMBL: M69214; AAA20488.1; ALT_SEQ.
CC DR PIR: S27656; S27656.
CC DR PIR: A43303; A43303.
CC DR Interfero: IPR003684; Porin_alpha.bac.
CC DR Pfam: PF02530; Porin_2; 1.
CC KW Outer membrane: Signal; Antigen.
CC FT SIGNAL 1 22
CC FT CHAIN 23 366 OUTER MEMBRANE PROTEIN IITA.
CC SEQ SEQUENCE 366 AA; 38969 MW; 6CC4A4E5CC91381 CRC64;

Query Match 13.4%; Score 140.1; DB 1; Length 366;
Best Local Similarity 17.4%; Pred. No. 23;
Matches 54; Conservative 17; Mismatches 36; Indels 203; Gaps 15;

QY 8 GYNNCGFYGYVNDGHC-----VTYINGPGGCGFSVMSNSGNF----- 45
DB 130 GFRAGLFYSWMDGLSGETDDIGSVTLHNSIRYQ-----ESGTFYAGLSVDELDGY 184
QY 46 -----VGCK-----GWC----- 52
DB 185 QGTFPTGVIPTGTTDTADDPNNVGVAFGIGTAGAFSYQVYGMDVNDGAIKRMGTV 244
QY 53 ---PGTKNKVINESSGYNPNNGNSYLSVYGSNRPLIEY-----YIVEN 92
DB 245 ELPGGT-----FGLAGYSSGPNSSYSSAEWA--VAAEYAIKATDKLTIPGRWHGVHPED 298
QY 93 FGTYNPSTGATKIGEVTSQSGSVYDIYRTQKRVNPSLTIGATFYQVYSVRNRHSSGSVNT 152
DB 299 F-----DG-----LGDA-----WKV----- 308
QY 153 ANHFNMAOQGLTIGTMDYQIV-----AVEGYESS----- 182
DB 309 -----GL-----TVDYQIVENFYAKASVOYLPDPQDGEDSTSGIFACSVSNHLVDAP 355
QY 183 ---GSASIT 188
DB 356 GLRIGSTTIS 365

RESULT 43
BIGA_SALTY STANDARD; PRT; 1953 AA.
ID BIGA_SALTY
AC P25927; P25928; Q9XCQ3;
DT 01-MAY-1992 (Rel. 22, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Putative surface-exposed virulence protein biga precursor.
GN BIGA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN 11
RN SEQUENCE FROM N.A.
RC STRAIN-ATCC 14028;
RA Stojiljkovic I., Valentine P., Heffron F.;
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN-LT2 / SGC1412 / ATCC 700720;
RX MEDLINE=21534948; Pubmed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT *Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.*;
RN Nature 413:852-856(2001).
RN [3]

RP SEQUENCE OF 1-765 FROM N.A.
RC STRAIN-LT2;
RX MEDLINE=91100301; Pubmed=1987123;
RA Wu J.Y., Siegel L.M., Kredich N.M.;
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:
RT requirement for a cloned cysG plasmid to overcome limiting streptome
RT cofactor.";
RL J. Bacteriol. 173:325-333(1991).
CC -1- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
CC in positions 414 and 732.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.lsb-slb.ch/announce/>
CC or send an email to license@lsb-slb.ch).

CC EMBL: AF133696; AAD39458.1; -
CC DR EMBL: AE008859; AAL22340.1; -
CC DR EMBL: M64606; AAA27042.1; ALT_FRAME.
CC DR EMBL: M64606; AAA27043.1; ALT_FRAME.
CC DR PIR: C39200; C39200.
CC DR PIR: D39200; D39200.
CC STYGene: SG10437; biga.
CC KW Virulence; Repeat; Signal; Complete proteome.
CC FT SIGNAL 1 27
CC FT CHAIN 28 1953
CC
CC DOMAIN 101 252
CC FT REPEAT 101 103
CC FT REPEAT 104 113
CC FT REPEAT 114 122
CC FT REPEAT 123 133
CC FT REPEAT 134 144
CC FT REPEAT 145 155
CC FT REPEAT 156 166
CC FT REPEAT 167 177
CC FT REPEAT 178 188
CC FT REPEAT 189 199
CC FT REPEAT 200 210
CC FT REPEAT 211 221
CC FT REPEAT 222 232
CC FT REPEAT 233 243
CC FT REPEAT 244 252
CC FT CONFLICT 207 207
CC FT CONFLICT 514 514
CC FT CONFLICT 1698 1698
CC FT CONFLICT 1795 1798
CC FT CONFLICT 1836 1837
CC SEQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C954D91AE CRC64;

Query Match 13.4%; Score 139.8; DB 1; Length 1953;
Best Local Similarity 16.9%; Pred. No. 5.1e+02;
Matches 62; Conservative 30; Mismatches 62; Indels 212; Gaps 17;

QY 7 TGINNC-----YFY-----SYNNDG----- 21
DB 1240 TFYNNDDFTGSIAGTSYQOEIVNTGDMTVAEDKSLVSGSFYFNEDEATLTLSGSAVEG 1299
QY 22 -----HGGVTYNGPGCGFSVMSNSGNFVG----- 47
DB 1300 GEMTITNLRANDSLQVNSGTTTATNGYSALTTVNGSDPKWMTATGAVINGINPDAP 1359
QY 48 ---GKGWPGTKNKVINESSGYNPNNGNSYLSVYGSNRPLIEYIVE--NFGTVNPSN- 100
DB 1360 LNLGRGYNEGNQ-----GTINVGDNAAVAISGTS-----YVINLVNSGTINWGRE 1407
QY 101 -----GATKLGVTSDG--SYV----- 115
DB 1408 QGKEDGTGCTGLIKGNMGNAATTINN-TADGVINVAADSVAFGCKTKAIINNGEINLLC 1466

OY 116 ----DIYRORVNOPIITGATFYQWVRNRH-----SSGSVNT----- 152
DB 1467 DSGCIVY-----ABGTGTCT-----QNDHNGTADIVIPDATATPTEGSIPTPPADP 1511
OY 153 -----ANHF-----NANAQGLTGTGMDYQVAVNEGYSS--- 182
DB 1512 NAAPOOLSNRYVGTNADSSGSLKANLVIGDNVKNVDTGTSATDTTAVVDNAFGSNIQ 1571
OY 183 GSASIT 188
DB 1572 GADNIT 1577
RESULT 44
WAPA_BACSU
ID WAPA_BACSU STANDARD: PRT: 2334 AA.
AC 007833:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 13-JUN-2002 (Rel. 41, Last annotation update)
DE Wall-associated protein precursor.
CN WAPA OR N17G.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE-93302506; Pubmed=8316082;
RA Foster S.J.;
RT "Molecular analysis of three major wall-associated proteins of
RT Bacillus subtilis 168: evidence for processing of the product of a
RT gene encoding a 258 kDa precursor two-domain ligand-binding
RT protein."
RL Mol. Microbiol. 8:299-310(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168 / BGSC1A1;
RX MEDLINE-95219088; Pubmed=7704263;
RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis
RT genome containing the hut and wapa loci."
RL Microbiology 141:337-343(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-168 / BGSC1A1;
RX MEDLINE-97124196; Pubmed=8969509;
RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
RA Miwa Y., Fujita Y.;
RT "Sequencing of a 65 kb region of the Bacillus subtilis genome
RT containing the hic and cel loci, and creation of a 177 kb contig
RT covering the gnt-sacX region."
RL Microbiology 142:3113-3123(1996).
CC -1- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
CC MOTILITY, SECRETION OR DIFFERENTIATION
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
CC INTO THE MEDIUM.
CC -1- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE
CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
CC MOTIF REPEATED 31 TIMES.
CC -1- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
CC SIMILARITY TO THE REPEAT IN E.COLI RBS GROUP OF PROTEINS (RBSA-D).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: L05634; AAA22883.1; -

DR EMBL: D31856; BAA06656.1; -
DR EMBL: D29985; BAA06260.1; -
DR EMBL: D83026; BAA11683.1; -
DR EMBL: 299124; CAB15959.1; -
DR PIR: S32920; S32920.
DR Subtilisin; BGI0797; WAPA.
DR Interpro: IPR003305; CBM_Cenc.
DR Pfam: PF02018; CBM_4_9; 1.
DR Cell wall; Repeat; Signal; Complete proteome.
DR OR 32 (POTENTIAL)
FT CHAIN 1 28
FT SIGNAL 1 28
FT DOMAIN 1021 2139
FT REPEAT 1021 1040
FT REPEAT 1042 1061
FT REPEAT 1063 1082
FT REPEAT 1083 1102
FT REPEAT 1109 1128
FT REPEAT 1129 1148
FT REPEAT 1150 1169
FT REPEAT 1174 1193
FT REPEAT 1199 1218
FT REPEAT 1219 1238
FT REPEAT 1246 1265
FT REPEAT 1267 1286
FT REPEAT 1290 1309
FT REPEAT 1312 1331
FT REPEAT 1350 1369
FT REPEAT 1374 1393
FT REPEAT 1419 1438
FT REPEAT 1456 1475
FT REPEAT 1490 1509
FT REPEAT 1511 1530
FT REPEAT 1532 1551
FT REPEAT 1575 1594
FT REPEAT 1620 1639
FT REPEAT 1640 1659
FT REPEAT 1661 1680
FT REPEAT 1687 1706
FT REPEAT 1727 1746
FT REPEAT 1753 1772
FT REPEAT 1795 1814
FT REPEAT 1820 1839
FT REPEAT 1840 1859
FT REPEAT 1861 1880
FT REPEAT 1887 1906
FT REPEAT 1908 1927
FT REPEAT 1929 1948
FT REPEAT 1969 1988
FT REPEAT 1983 2002
FT REPEAT 2008 2027
FT REPEAT 2028 2047
FT REPEAT 2051 2070
FT REPEAT 2071 2090
FT REPEAT 2093 2112
FT REPEAT 2120 2139
FT REPEAT 2134 2153
FT SEQUENCE 2334 AA; 258329 MW; B75138CCD278BAA3 CRC64;
Query Match 13.4%; Score 139.7; DB 1; Length 2334;
Best Local Similarity 8.8%; Pred. No. 7.1e+02;
Matches 84; Conservative 32; Mismatches 61; Indels 773; Gaps 25;
OY 8 GYNN-----GYFYSTW----- 18
DB 629 GYNNATGYFEDLSMKAVSATGYKVQVFNKGPFETIDLGNSWTKKGIPTSAEIK 688
OY 19 -----NGCHG----- 23
DB 689 AGKVALHKGSGELDPINGPITYKKNAGGOGAKRNYSFKIIAYNKDEALASPATPALP 748
OY 24 -----GVTVN----- 29
DB 749 DIARPKNVTVGLVNTKSSQTVYNLWEKVQNAKGYKVIYNGKEYQSFVDGADHWTT 808
OY 30 -----GGQGFVN-----MSN-SGNEVG----- 47
DB 809 QNKNIPTSEIKASYKLTHTDGGELALDPSVYNNANGVNKKKNSFTLVAVDANG 868
OY 48 ----- 47
DB 869 ETIPTAFNPFTHEGAFLCTEEYWSIIDIPSGOLGATGNTVINEEDLSIDGRGLGL 928

```

OY 48 -----GKGM-----QP----- 53
D 929 SRTYNSLSDSDHLFGGOWADAFETSYISIDGAMTIDEDATTHRTTKADGTQPPRGY 988
OY 54 ----- 53
D 989 LELLETADOFILTKDQTNAYFNKKGKGLQKVVDGHNNAVTYVYNDKNLTATIDASGRK 1048
OY 54 -----GTRKNVINF-----GYN----- 67
D 1049 LFTTYDENGHWYSITSPKNNKVTYSYENDLLKKVTDGTWTSYDSEGRVLYKQYSANS 1108
OY 68 -----PNCNSYLSYWGMSRNP 84
D 1109 TEAKPVFTEQYSGHRLKAIKAKKETVYVSYADKTKTLLMTPNGRKYQYGENAENP 1168
OY 85 -----IEY-----IYENFGT--- 95
D 1169 OVIDAEGKLTITNTKYEENNVEDVPNDVGTGKATESYQDKGNVTSVKDAYGTERTY 1228
OY 96 -YNSPTGATKL-----GEVT-----SDGSYYDIY----- 118
D 1229 ETNKNNDVTNMDTEGNVTDIAYGLDAVSETDQSGKSSAAVYDKYGMQIOSSKDLAS 1288
OY 119 ----- 118
D 1289 TNLKGSFEAKSGMNLASKDRRKISVIAKSGVLSGSKALEVLSQSTSACTDHGYS 1348
OY 119 RTQRY----- 123
D 1349 AOTFVLEPNTTYTLLSGIKITDLAKSRAVFNLDRDQKRIQIHNEYSALAGKNDWTK 1408
OY 124 -----NPSLIGATFY-----Q 136
D 1409 ROTFTTPANAGAAVYMEYDHRKDKGKAMFEVQLEKEVSSNPYONSSFTSARE 1468
OY 137 YNSRRNRHSSGSVNTANFN-----AWAOG-----LTIG 167
D 1469 NMNV-----SGASVDESEGNDDVSLKAARTSASQGSVTKQTVVLGOSANDKPYVLTLL 1523
OY 168 TW-----DYOIVAVEGY-----FSSGS-----ASTIV 189
D 1524 GMSKASSVKTDEKDYSLQANVTYADGSTGYNAKFPSTGQEWNRRAVY 1573

RESULT 45
GUN_BACS6
ID GUN_BACS6 STANDARD: PRT: 941 AA.
AC P19424;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
DE (Alkaline cellulase).
DE Bacillus sp. (strain KSM-635).
OC Bacteria: Firmicutes: Bacilliales: Bacillaceae: Bacillus.
OC NCBI_TaxID=1415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91037937; PubMed=2230718;
RA Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.;
RT "Molecular cloning and nucleotide sequence of a gene for alkaline
RT cellulase from Bacillus sp. KSM-635."
RL J. Gen. Microbiol. 136:1327-1334(1990).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
CC HYDROLASES).
CC -1- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
```

```

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M27420; AAA22304.1; -
DR PIR: S29043; S29043.
DR HSSP: 085465; 3A3H.
DR InterPro: IPR005086; CBM_17_28.
DR InterPro: IPR001347; GH_5.
DR InterPro: IPR001119; SLH.
DR Pfam: PF00150; cellulase. 1.
DR Pfam: PF00395; SLH; 3.
DR Pfam: PF03424; CBM_17_28; 2.
DR PROSITE: PS00659; GLYCOSYL_HYDROL_F5; 1.
DR PROSITE: PS01072; SLH_DOMAIN; 2.
KW Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 30 941
FT DOMAIN 40 99
FT DOMAIN 100 151
FT DOMAIN 152 225
FT ACT_SITE 373 373
FT ACT_SITE 485 485
FT ACT_SITE 485 485
SQ SEQUENCE 941 AA; 104628 MW; BEA2AC3B169BFADA CRC64;

Query Match 13.3%; Score 139.4; DB 1; Length 941;
Best Local Similarity 13.6%; Pred. No. 1,4e+02;
Matches 70; Conservative 26; Mismatches 61; Indels 356; Gaps 21;

OY 4 OPCTGYNNG----- 12
D 373 EFSPPNNGGRLTNDKCKEAYKEAEPYIEMLRKGDMMILVGNPNMSQRPDLASDNP 432
OY 13 -----YFYSYNDGHC-----GYTYTN 29
D 433 DAENIMYVHFYTGSHGASHIGYPECTPSERSNVANRYALDNGVAVFATBMGTQSQAN 492
OY 30 GPGGOF-----SYMMSNSGNGFYGKGGKQPGTKNV----- 59
D 493 GDGPGYFDEADVWLNFLNKHNISWAN-----WSTLNKEISGAFPFELGRTDAVD 543
OY 60 -----INSGSY-----NP 68
D 544 LDPGANQVAPBELSLSGEYVRARIKIETPTIDRTKFKLVWDFPDGTGQFQVNGDSP 603
OY 69 N-----GNSY-----LSYVGMSRN-----PLIEYIVE 91
D 604 NKESITLSNNNDALQIEGLNVSNDISEGNYMDNVRSLADGWSSENVLDGATELTIDVIVE 663
OY 92 N-----FGTNPSTGATKGLD-----VTSQGSYIDYRTOR 122
D 664 EPTTVSIAIIPQAPAGMANP-TRAIKVEDFEFSGPDGYKALVLTTSDDS----- 713
OY 123 VNQPSI-----IGTATF- 134
D 714 ---PSLETTATSPEDNTMSNILLFVGTEDADVYISLDNTVSGTEIEIYIHDEKGTATLP 770
OY 135 -----YOYWSYRRNRHSSG-----SVNTANHFNA-----WA----- 160
D 771 STFEDGTQCGWDM---HTSSGVKTAITIEANSMNLSMEYAVPEVKPSDGMATAPRLDF 827
OY 161 -QOGLTLGTMDOYIAVEGYF-----SSGSAST 187
D 828 WKDELVRGTSVY--ISFDYIDAIVRASGAIS 858

RESULT 46
VG37_BPK3
ID VG37_BPK3 STANDARD: PRT: 1243 AA.
AC Q38394;
DT 15-DEC-1998 (Rel. 37, Created)
```

DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Long tail fiber protein p37 (Protein Gp37) (Receptor recognizing
 DE protein).
 GN 37
 OS Bacteriophage K3.
 OC Viruses: dsDNA viruses, no RNA stage: Caudovirales: Myoviridae;
 OC unclassified Myoviridae.
 OX NCBI_TaxID=10674;
 RN 11
 RP MEDLINE=87112716; PubMed=3806672;
 RX Ride I., Drexler K., Eschbach M.-L., Henning U.;
 RA "DNA sequence of the tail fiber genes 37, encoding the receptor
 RT recognizing part of the fiber, of bacteriophages T2 and K3.",
 RL J. Mol. Biol. 191:255-266(1986).
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE DISTAL HALF TAIL FIBER. IT
 CC CONSTITUTES THE PART OF THE LONG TAIL FIBERS THAT RECOGNIZES THE
 CC BACTERIAL RECEPTOR.
 CC -1- SUBUNIT: THE DISTAL HALF-FIBER CONTAINS TWO MOLECULES EACH OF GP36
 CC AND GP37 AND ONE MOLECULE OF GP35.
 CC -1- MISCELLANEOUS: THE TWO GP37 PROTEIN CHAINS RUN IN PARALLEL, THE
 CC LENGTH OF THE DISTAL HALF-FIBER, WITH THE AMINO END NEAR THE
 CC CENTER KINK OF THE FIBER AND THE CARBOXYL END AT THE DISTAL TIP.
 CC THE OTHER POLYPEPTIDES ARE DISTRIBUTED UNIFORMLY ALONG THE LENGTH
 CC OF THE DISTAL HALF-FIBER.
 CC -1- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC EMBL: X04747; CAA28445.1; -
 DR Fiber protein.
 KW
 SO SEQUENCE 1243 AA; 132990 MW; 115E6B9D0C695928 CRC64;
 Query Match 13.3% Score 139.3; DB 1; Length 1243;
 Best Local Similarity 9.5% Pred. No. 2.3e+02;
 Matches 79; Conservative 25; Mismatches 61; Indels 667; Gaps 22;
 QY 3 IQPG-----TGYNNGYFYS----- 16
 DB 408 INPGLIKLVGSSNVQYADGNISIQPVKLDNELFLNSSNNTAGLFGAPSKVDGTRAI 467
 QY 17 YWNG-----H----- 22
 DB 468 QMNGGTREGONKNYVIKMGNSFNATGDRSRETVPQVSDSGYFYAHRKAPTGEDETI 527
 QY 23 -----GGVTYNG-----PGGQ----- 34
 DB 528 RIEQFAGELAKSINAVENKVGSLTVGGVTMSGMLNTGSSSITGVKIGCTYDAL 587
 QY 35 -----FSV----- 37
 DB 588 RIMNSRYCAIFRSETSLHIPTNENEGENCAINLRPFSTELGTGTVMCLHDVHLNSG 647
 QY 38 -----NM----- 39
 DB 648 SSTGLLOVNSLTKIKICPVLTINERNAALTLDSPSSSSANYLOGSKAGTKSMVYVGLGA 707
 QY 40 -----SNSGNF----- 45
 DB 708 GNDLSLTSQSYGHGLVSDNPNVSIKPLKGNQOLGDTGNTGSSGAFANLNTLANKVN 767
 QY 46 -----VGKGNQPGT----- 55
 DB 768 SGFTYGTATGMYKFAFATVTPQSTAFKIVGSGSGNSGLFTQCINIAEIVLRTGNBRPA 827
 QY 56 -----KKKVINFGSGSYNPNGNSY-LSVYGNRNPILIEYIVENGTY--- 96

DB 828 DLNAVLTRTIGAFKNIANV-----NVSQGTYYIYVA-----GTYCNO 867
 QY 97 ----- 96
 DB 868 LACEMACTENATISVIGINSTOSPVDDLPTAVANGOVANLNLVDSGCKRREASESEI 927
 QY 97 --NPSTG-----ATKICEVY-----SPGSYVDIYRTORVNOPSLIGTATFYQVSVRR-- 142
 DB 928 AINSQTGIRIRSNADKTKGSVATMLRNDGGSFYILFTDKNDTD---GAATVNGENSKRPF 984
 QY 143 -----NHRSSGSVN----- 151
 DB 985 AINLTGFEVMNNGIAVRSALFYNSINVDNGSINFDKSGANRMRIFHAGDASRCNR 1044
 QY 152 -----TANHF-----NANAQGLTIGTYDYQ 172
 DB 1045 IEIADETNYIAFEKABGAGANRFVNNATVSGVNQMSFGVNTSNALGNSITFGPDYTG 1104
 QY 173 I-----VAVEGYF----- 180
 DB 1105 IKONGDGLDIYANNAQYFRQNGDLXSYKNINAPNYIISDITKSNFRIENALDKVE 1164
 QY 181 -----SSGSASITVS 190
 DB 1165 KLVGVYDKAEYIGGEAIEIEAGIYAOTLDVLPBEAVRETEDSKNIKLTIVS 1216
 RESULT 47
 FHUE.ECOLI
 ID FHUE.ECOLI STANDARD; PRT; 729 AA.
 AC P16869; P77292;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FhuE receptor precursor (outer-membrane receptor for Fe(III)-coprogen,
 DE Fe(III)-ferrioxamine B and Fe(III)-rhodotulic acid).
 GN FHUE OR B1102.
 OS Escherichia coli.
 OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 CX 11
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=90286919; PubMed=2162465;
 RA Sauer U., Hantke K., Braun V.;
 RT "Sequence of the fhuE outer-membrane receptor gene of Escherichia
 RL coli K12 and properties of mutants";
 RL Mol. Microbiol. 4:427-437(1990).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley H., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12";
 RL Science 277:1453-1474(1997).
 RN 131
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajinara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitegawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiiuchi T.;
 RT "A 7.18-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 12.7-28.0 min region on the linkage map";
 RL DNA Res. 3:137-155(1996).

```

RN [4]
RP SEQUENCE OF 37-50.
RC STRAIN-K12:
RX MEDLINE-87194585; PubMed-3032906;
RA Sauer M., Hantke K., Braun V.;
RT "Ferric-coprogen receptor FhuE of Escherichia coli: processing and
RT sequence common to all TonB-dependent outer membrane receptor
RT proteins.";
RL J. Bacteriol. 169:2044-2049(1987).
CC -1- FUNCTION: REQUIRED FOR THE UPTAKE OF IRON(III) VIA COPROGEN,
CC FERRIOXAMINE B, AND RHODOTURULIC ACID.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- INDUCTION: FOR INDUCTION THE TONB AND THE EXBB PROTEIN HAVE TO
CC BE ACTIVE.
CC -1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X17615; CA35616.1; -
DR EMBL: AE000210; AAC74186.1; -
DR EMBL: D90745; BAA35909.1; -
DR EMBL: D90746; BAA35917.1; -
DR PIR: S09262; S09262.
DR PIR: A26875; A26875.
DR EcoGene: EG10306; fhuE.
DR InterPro: IPR000531; TonB_box.
DR Pfam: PF00593; TonB_box.
DR PROSITE: PS00430; TONB-DEPENDENT_REC_1; 1.
DR PROSITE: PS01156; TONB-DEPENDENT_REC_2; 1.
DR Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor;
KW Complete proteome.
FT SIGNAL 1 36
FT CHAIN 37 729 FHU RECEPTOR.
FT SITE 42 49 TONB BOX.
FT SITE 712 729 TONB C-TERMINAL BOX.
FT MUTAGEN 44 44 V->P: ABOLISHES TRANSPORT ACTIVITY.
FT MUTAGEN 46 46 V->P: ABOLISHES TRANSPORT ACTIVITY.
FT MUTAGEN 163 163 G->A,V,N,D,H: IMPAIRED TRANSPORT AND
FT GROWTH.
FT CONFLICT 363 363 G->C (IN REF. 1).
FT SEQUENCE 729 AA; 81232 MW; 68ACE7D110F76CD CRC64;
SO Query Match 13.3%; Score 139; DB 1; Length 729;
Best Local Similarity 14.1%; Pred. No. 90;
Matches 73; Conservative 20; Mismatches 70; Indels 353; Gaps 19;
OY 8 GYNN-----GYFY-----YWN-DG- 21
DB 227 GYNNDSWLDRYNSEKTFEFGIVDADGLDGLTLTSAGYEYGRIDVNSPTWGLPWRNTDGS 286
OY 22 -----IGV-----TYT 28
DB 287 SNSYDRASAPDMAYNDKEINKVFMTLKQOFADTQWATLMTATSEVEFSKMYVDAYV 346
OY 29 NGPGGFSVNNNSNG---NFVGKGKMGPGTNNKV-----INFGSSY 66
DB 347 NKADGMLVGPYSNYGPGFDYVGCTGCMNSG-KRKYDALDLFADGSYELFGRHNLMEFGSSY 405
OY 67 NPNGNSYLSVYG-----MSRNPLE----- 86
DB 406 SKONNRFFSWANIFPDEIGSFYNFNGNFPQTDMSPOSILADDDTTHMKSLYAATFVTLAD 465
OY 87 -----YYIENGTYNPSI----- 100
DB 466 PLHLILGARITNNWRVDLTLYSMENKHTTTPYAGLVFLIDNMWSTYASYSIFOPONDRDSS 525
OY 101 ----- 100

```

```

DB 526 GKYLAPITGNNYELGKSDMWSRLTTLAIFRIEQDNVAOSTGPIPGSNGETAYKAVD 585
OY 101 -----GATK-----LGE 107
DB 586 GTVSKGVEEFLNGAITDMMQLTFGATRYIAEDNMGNAVNPMLPRTTYKMTFSYRLPVME 645
OY 108 VTSQGSV-----YDIYRTORVNQPS--IIIGTATFYQWGVRRHRSSGSVNTANH 155
DB 646 LTVGGGVWQNRKYVTDTPYTGTFRAEDGSIALVDLFTFRYO---VTKNFSLQGNVN--NL 700
OY 156 FNMAAOGELTGTMDYQIVAVEG---YFSSGSASIT 188
DB 701 FDK-----TYD---TWVEGSIYVGTPEPNFSIT 724

```

RESULT 48

```

GUXB_CELFI
ID GUXB_CELFI STANDARD: PRT; 1090 AA.
AC P50899;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Exoglucanase B precursor (EC 3.2.1.91) (Exocellulohydrolase B)
DE (1,4-beta-cellulohydrolase B) (CBP120).
GN CBHB OR CENE.
OS Cellulomonas fimi.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Micrococccineae; Cellulomonadaceae; Cellulomonas.
OX NCBI_TaxID=1708;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 456-461.
RC STRAIN=ANCC 484;
RX MEDLINE-96003898; PubMed-7575482;
RX Shen H., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
RT "Cellulohydrolase B, a second exo-cellulohydrolase from the
RT cellulytic bacterium Cellulomonas fimi.";
RL Biochem. J. 311:67-74(1995).
RN [2]
RP SEQUENCE OF 54-75.
RX MEDLINE-93209933; PubMed-8458833;
RX Melnke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
RT "Cellulose-binding polypeptides from Cellulomonas fimi: endoglucanase
RT D (Cend), a family A beta-1,4-glucanase.";
RL J. Bacteriol. 175:1910-1918(1993).
RN [3]
RP SEQUENCE OF 54-78.
RX MEDLINE-94197708; PubMed-8147863;
RX Shen H., Tomme P., Melnke A., Gilkes N.R., Kilburn D.G.,
RX Warren R.A.J., Miller R.C. Jr.;
RT "Stereochanical course of hydrolysis catalysed by Cellulomonas fimi
RT Cend, a member of a new family of beta-1,4-glucanases.";
RL Biochem. Biophys. Res. Commun. 199:1223-1228(1994).
CC -1- FUNCTION: HYDROLYSES CELLOHEXAOSE TO A MIXTURE OF CELLOTETRAOSE,
CC CELLOTRIOSE AND CELLOBIOSE, WITH ONLY A TRACE OF GLUCOSE. IT
CC HYDROLYSED CELLOPENTAPOSE TO CELLOTRIOSE AND CELLOBIOSE, AND
CC CELLOTETRAOSE TO CELLOBIOSE, BUT IT DID NOT HYDROLYSE CELLOTRIOSE.
CC HAS ALSO WEAK ENDOGLUCANASE ACTIVITY. HYDROLYSES GLUCOSIDIC BONDS
CC WITH INVERSION OF ANOMERIC CONFIGURATION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC in cellulose and cellobiose, releasing cellobiose from the non-
CC reducing ends of the chains.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
CC (CBD).
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY L (FAMILY 48 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: L38827; AAB00822.1; -
 DR HSSP: P07986; 1EXG.
 DR InterPro: IPR001919; Bac_cellose-blnd.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003962; FNIII_repeat.
 DR InterPro: IPR000556; Glyco_hydro_48.
 DR Pfam: PF00041; fn3; 3.
 DR Pfam: PF00553; CBM_2; 1.
 DR Pfam: PF02011; Glyco_hydro_48; 1.
 DR PRINTS: PR00014; FNTYPEIII.
 DR PRINTS: PR00844; GLHYDRASE48.
 DR ProDom: PD011903; Glyco_hydro_48; 1.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS00561; CBD_BACTERIAL; 1.
 KM Cellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.
 FT SIGNAL 1 33
 FT PROPEP 34 53
 FT CHAIN 54 1090
 FT DOMAIN 54 699 EXOGLUCANASE B.
 FT DOMAIN 700 785 CATALYTIC (BY SIMILARITY).
 FT DOMAIN 794 884 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 891 978 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 989 1090 FIBRONECTIN TYPE-III 3.
 FT ACT_SITE 513 513 CELLULOSE-BINDING (BY SIMILARITY).
 FT DISULFID 990 1089 NUCLEOPHILE (BY SIMILARITY).
 SO SEQUENCE 1090 AA; 114829 MW; 046BBD956F2F399 CMC64;

Query Match 13.3%; Score 138.7; DB 1; Length 1090;
 Best Local Similarity 11.5%; Pred. No. 1.9e+02;
 Matches 69; Conservative 34; Mismatches 76; Indels 423; Gaps 19;

OY 8 GYNGY-----FYSYMDGNGCYT----- 26
 DB 383 GYGNPLAANALSTDPLKTPSPAKADMAASMOROLEFTYTLQASNGLAGATNSWDGA 442
 OY 27 -----YTNCP----- 31
 DB 443 YAOPTGPTFYGMGTETAPVYDPPSRNFMGMQAMGVORVALYLYASGNAOKKILLDKW 502
 OY 32 -----GGSFSV-----NMSN-----SGN----- 44
 DB 503 VPMVAVANISTDGAASMKVPSLELKTGKPRDTWMAAAPTGNGLFVEVTSYGDGVAAADTAR 562
 OY 45 ---FVGKGMQPGTKK----- 67
 DB 563 ALLFYAAKSGDTASRKAKALDAIWAANNODPLGSAVETRGDYKRPDDTYVANGGCIYI 622
 OY 68 PN-----GNSYLSVY-----GMSR----- 81
 DB 623 PSCWMTGMPNGDVIKRGVSEFLDIRSFYKDPNMSKYQTLFDGGAEPQFRHRTMAQTAVA 662
 OY 82 NPLIEIYIYENCTYVPS-----GA 102
 DB 683 GALADYARLFDDGTTPTTAPTPTVPTGLAGVVTSTEATISWTASTDTRVTGYDYVRA 742
 OY 103 TKLG-----E 107
 DB 743 TKVGTATTTSTFDTGLTASTAVAYTVRAADAGNVSAPSALTVTTKAPPSDTTASVPA 802
 OY 108 VTSDCSV-----YDIYR-TORVNQPSI-----IGTATFYQY 137
 DB 803 ITSSSTANSVTIGMSASTDNMGSGLAGYDVRGATRAQTALTFTDTGLTASTAYEY 862
 OY 138 ----- 137
 DB 863 TVRADVAGNSAPSTAVSYTKSDTTPDTTASVPAGLAAMVTETSAALTWNASTDNG 922
 OY 138 -----WVYRRNRSSGSVNTANHFANMAOGLTGT-KDYQVAVNE--GYFSSGSAST 188
 DB 923 GSGLKGYDVRGATRVGSTTTA-----SYDTGTLTATTAVOYTVRATDNAGNVSASAALS 978

OY 189 VS 190
 DB 979 VT 980

RESULT 49
 FAND_ECOLI
 ID FAND_ECOLI STANDARD; PRT; 783 AA.
 AC P12050;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Outer membrane usher protein fand precursor.
 GN FAND.
 OS Escherichia coli.
 OC Plasmid pFK99.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B41;
 RX MEDLINE=89160266; PubMed=2564179;
 RA Roosendaal B., Bakker D., de Graaf F.K.;
 RT "The nucleotide sequence of the fand gene encoding the large outer
 membrane protein involved in the biosynthesis of K99 fimbriae.";
 RL Nucleic Acids Res. 17:1263-1263(1989).
 RN [2]
 RP SEQUENCE OF 1-20 FROM N.A.
 RA Roosendaal B., Gaastria W., de Graaf F.K.;
 RT "The nucleotide sequence of the gene encoding the K99 subunit of
 RT enterotoxigenic Escherichia coli.";
 RL FEMS Microbiol. Lett. 22:253-256(1984).
 RN [3]
 RP SEQUENCE OF 770-783 FROM N.A.
 RC STRAIN-B41;
 RX MEDLINE=91312125; PubMed=1713284;
 RA Bakker D., Vader C.E.M., Roosendaal B., Mool F.R., Oudega B.,
 RA de Graaf F.K.;
 RT "Structure and function of periplasmic chaperrone-like proteins
 RT involved in the biosynthesis of K88 and K99 fimbriae in
 RT enterotoxigenic Escherichia coli.";
 RL Mol. Microbiol. 5:875-886(1991).
 CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF K99 FIMBRIAL
 CC SUBUNITS ACROSS THE OUTER MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
 CC (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: X13560; CAA1911.1; -
 DR EMBL: M35282; -; NOT_ANNOTATED_CDS.
 DR EMBL: X56001; CAA39473.1; -
 DR PIR: S02755; S02755.
 DR InterPro: IPR000015; Fimb_usher.
 DR Pfam: PF00577; usher; 1.
 DR PROSITE: PS01151; FIMBRIAL_USHER; 1.
 KM Outer membrane; Transmembrane; Fimbria; Transport; Signal; Plasmid.
 FT SIGNAL 1 23
 FT CHAIN 24 783
 FT DISULFID 763 782
 SO SEQUENCE 783 AA; 87156 MW; 23BDE3923A9B7069 CRC64;

Query Match 13.3%; Score 138.5; DB 1; Length 783;
 Best Local Similarity 14.9%; Pred. No. 1.1e+02;

Matches 71; Conservative 23; Mismatches 69; Indels 315; Gaps 20;

QY 9 YNNGYFYWMDGHC-----GVTYTN----- 29

DB 192 YGKGYKE-----HDKFTTDDVTLSPRAIKSLBGDLIIIGDTYNTSLMDNISFYVOLRSN 246

QY 30 -----GP----- 31

DB 247 NAMTPRRDGYPIISIGIAKSNARVYVKONGVYLHSELVSPGFPHINNRGIRSGELVMT 306

QY 32 ---GGQ-----FSYWNMSNGNF-----VGK--GMQPC----- 54

DB 307 VTEEDSEQOTRIPYFIANLLSPGNYNYDFGINKKEATWEPDNIPAGSFDYGLNLT 366

QY 55 -----TKNV-----INFGSYNPG 70

DB 367 NASLFEQHSNAGICAVSIGSLGAVSYSGNISRAKNODETDQGYSTANYSKNGANG 426

QY 71 -----NSLYSGMSRNP 84

DB 427 NLQIIKFSSEGYTOYANFDYRAPRKDKKEKEVEVTLTQCPASNVFLSVTKMKK----- 483

QY 85 IEY-----IVENFTYNS-IGATKLGCVTSDGSYYDIYRQRVNQPSTIGT 131

DB 484 --FYMNDNSVTGANVSYTQNFGTVNASVNGSYSRG---DGAKSDYMLGFNINIPFRHND 537

QY 132 AFYQYWSYVRNRHSSG-----SYNTA----- 153

DB 538 RQFYNSGTYTN-RNSGIGFAGFSEDYTKENYVNAALAKDNESVSLSTNTSSMFT 596

QY 154 -----NHFNMAQ-OGLTGTMD-----VOIVAVEG-FSSGSAS 186

DB 597 SASVSKNRSTNASQIGAILGVKDGWLTSMSSNSVALYQMEGLAGAFINGVES 654

RESULT 50

PM19.CHLPN STANDARD; PRT; 947 AA.

ID PM19.CHLPN Q92813; Q9USE2;

AC 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Probable outer membrane protein pmp19 precursor (Polymorphic membrane protein 19).

GN PMP19 OR CPN0539 OR CP0213.

OS Chlamydia pneumoniae (Chlamydia pneumoniae).

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

NCBI_TaxID=83558;

RN 11

RP SEQUENCE FROM N.A.

RC STRAIN-CML029;

RX MEDLINE-99206606; PubMed-10192388;

RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;

RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis"; Nat. Genet. 21:385-389(1999).

RT [2]

RP SEQUENCE FROM N.A.

RC STRAIN-AR39;

RX MEDLINE-20150255; PubMed-10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwin M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;

RT "Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).

RT [3]

RP SEQUENCE FROM N.A.

RC STRAIN-J138;

RX MEDLINE-20330349; PubMed-10871362;

RA Shirai M., Hiraoka H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,

RA Shirai T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;

RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CML029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).

RT [4]

RP SEQUENCE FROM N.A.

RC STRAIN-J138;

RX MEDLINE-20298986; PubMed-10839753;

RA Shirai M., Hiraoka H., Ouchi K., Tabuchi M., Kishi F., Kimoto M., Takeda H., Nishida J., Shibata K., Fujiwara R., Yoneda H., Matsushima H., Tanaka C., Furukawa S., Mura K., Nakazawa T., Ishii K., Shirai T., Hattori M., Kuhara S., Nakazawa T.;

RT "Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of Chlamydia pneumoniae isolates from Japan and the United States."; Infect. Dis. 181 Suppl 3:S524-S527(2000).

CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).

CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: AE001638; AAD18679.1; -;

CC EMBL: AE002181; AAF38083.1; -;

CC EMBL: AP002547; BAA98745.1; -;

CC HSSP: 090121; 1KPT.

DR TIGR: CP0213; -;

DR InterPro: IPR003368; Chlamydia_PMP.

DR InterPro: IPR003357; OMP.

DR Pfam: PF02385; OMP; 1.

DR Pfam: PF02415; DUF145; 1.

KW Outer membrane; Signal; Multigene family; Complete proteome.

FT SIGNAL 1 19

FT CHAIN 20 947

FT CONFLICT 453 453 E -> D (in Ref. 3).

SQ SEQUENCE 947 AA; 103642 MW; 20CE1DEE1606DF CRC64;

Query Match 13.2%; Score 138; DB 1; Length 947;

Best Local Similarity 16.8%; Pred. No. 1 6e+02;

Matches 62; Conservative 29; Mismatches 69; Indels 210; Gaps 14;

QY 6 GTGYNNGYFYSY-----WMDHGQVTVTNGPGQFSYWNMSNGNFYVGKGM 51

DB 600 GYGQGSWEFSWSPNDTKREKTTIASWT-----PTGFFSLDPKRRGSFIFTTLM 648

QY 52 QGCTKKKXVNFSG--SYNPGNSYLS-----YVG-----WSNPPLI 85

DB 649 S-----TFSGMLTASINIVNNVNNSEVPLQHLGVFGGVQYQIMEQNPQSSNNLL 700

QY 86 EYIYVNFGTYNP-----STGATKLGCVTSDGSYYDIYRQRVNQPSTIGATFYQYW 138

DB 701 VQHGAGNVARIPFSRNTLLSALTLTDLFSSSSQONVADKSHAO-----ILIGTVSLKSW 755

QY 139 ---SVR-----RNHRSSGSVNTA----- 153

DB 756 QALSLRSSFSYTEDSQVMKHVPYKGTSGSMRWGSSGVSYVPGIRYLKMTPEV 815

QY 154 ----- 153

DB 816 DLQYTKLVONPEVGYDPRFSSSEPTNLSPDIGALEMRFTGSRSLFLQVSTSYIKD 875

QY 154 -----NHFNMAQOGLTGL-----TMDYOIVAV-----EGYF 180

DB 876 LRRVNPQSSASLVLNHY-TWDLQGVPLGKEALNTLNTLTKIKIYVAYWGISTOREGSN 934

QY 181 SSGSASITVS 190

Tue Jul 1 13:01:52 2003

us-09-990-874-16.rsp

Page 34

Db 935 LSANAHGLS 944

Search completed: July 1, 2003, 11:49:29
Job time : 17 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 11:47:35 ; Search time 78 Seconds
(without alignments)
501.910 Million cell updates/sec

Title: US-09-990-874-16
Perfect score: 1045
Sequence: 1 OTIOPGTGNNGYFSYWNMD.....YQIVAVEGFSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organella:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-vertebrate:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	223	002244	002244 trichoderma
2	1033	98.9	223	099015	099015 trichoderma
3	876	83.8	223	090VF9	090VF9 trichoderma
4	767.8	73.5	241	012580	012580 chaetomium
5	705.9	67.6	219	012579	012579 chaetomium
6	702.5	67.2	232	09HEA4	09HEA4 aspergillus
7	696.9	66.7	290	09HEZ0	09HEZ0 phanerochaete
8	696.9	66.7	290	09HEY9	09HEY9 phanerochaete
9	688.5	65.9	295	09CIR2	09CIR2 fusarium ox
10	682.5	65.3	227	000263	000263 ascochyta p
11	678.9	65.0	227	09UVZ3	09UVZ3 helminthosp
12	665.9	63.7	225	08TG22	08TG22 aspergillus
13	656.8	62.9	221	09UUG2	09UUG2 penicillium
14	647.9	62.0	223	09HFO0	09HFO0 penicillium
15	635.9	60.9	231	013447	013447 coccollobolus
16	632.9	60.6	346	08VUT4	08VUT4 pseudomonas

17	631.3	60.4	221	3	P87037	P87037 aspergillus
18	628.9	60.2	231	3	000350	000350 coccollobolus
19	624.4	59.8	194	3	P81536	P81536 bacillomycete
20	615.9	58.9	227	3	09HCE1	09HCE1 humicola gr
21	613.9	58.7	283	3	096UV7	096UV7 lentitula e
22	611	58.5	335	2	09ROB8	09ROB8 cellulomona
23	610.7	58.4	335	2	008346	008346 streptomyces
24	610.7	58.4	335	2	09RMM4	09RMM4 streptomyces
25	608.7	58.2	338	2	056265	056265 thermomonus
26	606.9	58.1	231	3	09CIR1	09CIR1 fusarium ox
27	601.4	57.6	228	2	09S962	09S962 streptomyces
28	597.4	57.2	335	16	09RKN6	09RKN6 streptomyces
29	596.8	57.1	216	3	074716	074716 claviceps p
30	594.5	56.9	329	2	09RMM9	09RMM9 streptomyces
31	568.6	54.4	191	2	09EH89	09EH89 streptomyces
32	540.9	51.8	661	2	056674	056674 pseudomonas
33	536.3	51.3	241	16	09R172	09R172 streptomyces
34	532.9	51.0	361	2	052375	052375 caldicellul
35	530.9	50.8	656	2	059300	059300 cellvibrio
36	528.9	50.6	360	2	P77853	P77853 dictyoglomu
37	527.4	50.5	240	2	056013	056013 streptomyces
38	527.3	50.5	210	16	09KEP3	09KEP3 bacillus ha
39	524	50.1	357	2	08VP72	08VP72 pseudomonas
40	518.3	49.6	211	2	043993	043993 aeromonas p
41	514.2	49.2	213	2	08YVC3	08YVC3 bacillus sp
42	509.7	48.8	213	2	09ZB36	09ZB36 bacillus su
43	506.2	48.4	213	2	059254	059254 bacillus su
44	505.2	48.3	213	2	059256	059256 bacillus sp
45	505	48.3	217	5	097402	097402 phaeodon coc

ALIGNMENTS

RESULT 1	002244	PRELIMINARY:	PRT:	223 AA.
ID	002244			
AC	002244:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Endoxylanase II.			
GN	XLN2.			
OS	Trichoderma reesei (Hypocrea jecorina).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreales; Hypocreaceae; Hypocrea.			
OX	NCBI_TaxID=51453;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:94088442; PubMed-8264524;			
RA	Saarelainen R., Palohelmo M., Fagerstrom R., Suominen P.L.,			
RA	Nevalainen K.M.;			
RT	"Cloning, sequencing and enhanced expression of the Trichoderma reesei			
RT	endoxylanase II (PI 9) gene xln2.";			
RL	Mol. Gen. Genet. 241:497-503(1993).			
DR	EMBL: S67387; AAB29346.1.;			
DR	HSSP: P36217; IXYO.			
DR	InterPro: IPR001137; GH_11.			
DR	PIfam: PF00457; Glyco_hydro_11; 1.			
DR	PRINTS: PR00911; GLHYDRLASE11.			
DR	PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.			
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
KW	Glycosidase; Hydrolase; xylan degradation.			
SO	SEQUENCE 223 AA; 24069 MW; 79668149EDDA22F9 CRC64;			
Query Match	100.0%; Score 1045; DB 3; Length 223;			
Best Local Similarity	100.0%; Pred. No. 5.1e-36;			
Matches 190; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 OTIOPGTGNNGYFSYWNMDGCGVYTTNGPCGFSYWNMSNGNRYGCGKMPGTRKNKYI 60			
DB				
	34 OTIOPGTGNNGYFSYWNMDGCGVYTTNGPCGFSYWNMSNGNRYGCGKMPGTRKNKYI 93			

```
QY 61 NFSGSLPNPNCNSLYSVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
DB 94 NFSGSLPNPNCNSLYSVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 153
QY 121 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNANAAOGLTGTMDYQIVAVEGYF 180
DB 154 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNANAAOGLTGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 2
ID 099015 PRELIMINARY: PRT: 223 AA.
AC 099015:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Beta-xylanase precursor.
GN XYN2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=QM 6A.
RX MEDLINE=97076932; PubMed=8975597;
RA Grange D.C., Pretorius I.S., van Zyl W.H.;
RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
RT Saccharomyces cerevisiae."
RL Appl. Environ. Microbiol. 62:1036-1044(1996).
DR EMBL: U24191; AAB50278.1; -
DR HSSP: P36217; 1XVO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLYCDRLASE11.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 33
FT CHAIN 34 223
FT SEQUENCE 223 AA; 23981 MW; F696E545DAC90EB4 CRC64;

Query Match 98.9%; Score 1033; DB 3; Length 223;
Best local Similarity 98.9%; Pred. No. 1.6e-35;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYVWMDHGCVTYTNGPGQSFVNMNSGNEFVGKGMOPGTKNKYI 60
DB 34 QTIQPGTGNNGYFYVWMDHGCVTYTNGPGQSFVNMNSGNEFVGKGMOPGTKNKYI 93
QY 61 NFSGSLPNPNCNSLYSVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
DB 94 NFSGSLPNPNCNSLYSVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 153
QY 121 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNANAAOGLTGTMDYQIVAVEGYF 180
DB 154 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNANAAOGLTGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 3
ID 090VE9 PRELIMINARY: PRT: 223 AA.
AC 090VE9:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
```

```
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
OS Trichoderma viride.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Mitosporic Hypocreales; Trichoderma.
OX NCBI_TaxID=5547;
RN [1]
RP SEQUENCE FROM N.A.
RA Furman-Matarasso N., Cohen E., Avni A.;
RT "Mutations in the Active Site of the Ethylene Inducing Xylanase
RT Elicitor Inhibits the b-1-4-Endoxylanase Activity But Not the
RT Elicitation Activity."
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ012718; CAB60757.1; -
DR HSSP: P48793; 1XND.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLYCDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 33
FT CHAIN 34 223
FT SEQUENCE 223 AA; 24230 MW; FBFB12028FB1212A CRC64;

Query Match 83.8%; Score 876; DB 3; Length 223;
Best local Similarity 82.1%; Pred. No. 4.7e-29;
Matches 156; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYVWMDHGCVTYTNGPGQSFVNMNSGNEFVGKGMOPGTKNKYI 60
DB 34 QTIQPGTGNNGYFYVWMDHGCVTYTNGPGQSFVNMNSGNEFVGKGMOPGTKNKYI 93
QY 61 NFSGSLPNPNCNSLYSVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
DB 94 NFSGSLPNPNCNSLYSVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 153
QY 121 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNANAAOGLTGTMDYQIVAVEGYF 180
DB 154 QRVNPSIIGTATFTFYQWMSVRNRHRRSSGSVNTANHNANAAOGLTGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 4
ID 012580 PRELIMINARY: PRT: 241 AA.
AC 012580:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Endo-beta-1,4-xylanase (EC 3.2.1.8).
GN CGXB.
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Chaetomiaceae; Chaetomium.
OX NCBI_TaxID=47794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96118924; PubMed=8595661;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
RT "Two family G xylanase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans."
RL Curr. Genet. 29:73-80(1995).
DR EMBL: D49851; BAA08650.1; -
DR HSSP: P36217; 1XVO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLYCDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
FT SIGNAL 241 AA; 25564 MW; DCD4B012272F77F CRC64;
```

RESULT	5			
Q12579		PRELIMINARY:	PRT;	219 AA.
ID	Q12579			
AC	Q12579;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Endo-beta,4-xylanase A (EC 3.2.1.8).			
GN	CGXA.			
OS	Chaetomium gracile.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Sordariales; Chaetomiales; Chaetomiaceae; Chaetomium.			
OX	NCBI_TaxID=47794;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:96118924; PubMed=8359561;			
RA	Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;			
RT	"Two family G xylanase genes from Chaetomium gracile and their			
RT	expression in Aspergillus nidulans.";			
RL	Curr. Genet. 29:73-80(1995).			
DR	EMBL; D49850; BAA08649.1; .			
DR	HSSP; P36217; 1XO.			
DR	InterPro: IPR001137; GH_11.			
DR	Pfam; PF00457; Glyco_hydro_11; 1.			
DR	PRINTS; PR00911; GLHYDRLASE11.			
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.			
DR	Glycosidase; Hydrolase; Xylan degradation.			
QO	SEQUENCE 219 AA; 23324 MW; 479299E08FD9FBA CRC64;			

RESULT 6			
Q9HFA4			
ID	Q9HFA4	PRELIMINARY:	PRT: 232 AA.
AC	Q9HFA4;		
DT	01-MAR-2001 (Tremblrel, 16, Created)		
DT	01-MAR-2001 (Tremblrel, 16, Last sequence update)		
DT	01-JUN-2002 (Tremblrel, 21, Last annotation update)		
DE	xylanase G2 (EC 3.2.1.8).		
GN	XYNG2.		
OS	Aspergillus oryzae.		
OC	Eukaryota: Fungi: Ascomycota: Pezizomycotina: Eurotiomycetes:		
OC	Eurotiiales: Trichocomaceae: mitosporic Trichocomaceae, Aspergillus.		
OX	NCBI_Taxid=5062;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kimura T., Sakka K., Ohmiya K.;		
RT	"Molecular cloning, overexpression, and purification of major xylanase		
RT	from Aspergillus oryzae."		
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.		
SR	EMBL: AB044941; BAB20794.1; -		
DR	HSSP: P36217; IXYO.		
DR	InterPro: IPR001137; GH_11.		
DR	Pfam: PF00457; Glyco_hydro_11; 1.		
DR	PRINTS: PR00911; GLHYDRASE11.		
DR	PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.		
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.		
KW	Glycosidase; Hydrolase.		
SO	SEQUENCE 232 AA; 24605 MW; 1F73104751EA561C CRC64;		

[illegible]

RESULT 7		
ID	NAME	PROT; 290 AA.
09HEZ0	PRELIMINARY;	
AC	09HEZ0;	
DT	01-MAR-2001 (TEMBLrel, 16, Created)	
DT	01-MAR-2001 (TEMBLrel, 16, Last sequence update)	
DT	01-JUN-2002 (TEMBLrel, 21, Last annotation update)	
DE	Endo-1,4-B-xylanase B.	
CN	XYNB.	
OS	Phanerochaete chrysosporium.	
OC	Eukaryota: Fungi; Basidiomycota: Hymenomycetes; Homobasidiomycetes;	
OC	Apophialophorales; corticiaceae; Phanerochaete.	
OX	NCBI_TaxID=5306;	
RM	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=ME446;	
RA	Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;	
RT	"Molecular characterization and expression analysis of two endo-1,4-B-	
RT	xylanase genes from Phanerochaete chrysosporium."	
RL	Submitted (AUG-2000) to the EMBL/genbank/DBJ databases.	
DR	EMBL; AF301904; AAC4494.1; -.	
DR	HSSP; P00725; 1A26.	
DR	InterPro: IPR000254; CBD_fungal.	

RN [1]
RP SEQUENCE FROM N.A.
RA Kimura T., Sakka K., Ohmura K.;
RT "Acidophilic xylanase A from *Penicillium* sp. 40";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB035540; BAA86421.1; -.
DR HSSP: P36217; 1XTO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 221 AA; 24171 MW; 98BDD5BCBEC860AD CRC64;

Query Match 62.9%; Score 656.8; DB 3; Length 221;
Best Local Similarity 61.8%; Pred. No. 5e-20;
Matches 118; Conservative 30; Mismatches 41; Indels 2; Gaps 2;

OY 1 QTIDPG-IGYNNGYRYTWNHGHGVTYTNPGGQFYSVMNSNGNFVGKGNQPGTKNKV 59
DB 32 QTITSSQGTGNGNGYSEFTNGCGTVOYTNGAAGEYVTWENCDFTSKGKMGTSQA-RD 90
OY 60 INFSGSYNPNNGNSYLSYVGMNRNPLEEYIVENFGTYPNSTGATKLGVTSGSYVDIYR 119
DB 91 ITFEGTFNPSGNAYLAVGWTSPLEVEYILEDYGDYNGNSMTYKGTVSDGSVYDIYE 150
OY 120 TORVNOPSLIGTATFYQYWSVRNRHSSGSVNTANHFNMAAOGLTLGTMQIYAVEGY 179
DB 151 HQOVNOPSISGTATFNQYWSIRNQTSSGVTYTNHFNMAKLGNLGSFNQIYVSTEGY 210
OY 180 FSSGSASTIVS 190
DB 211 ESSGSSSTIVS 221

RESULT 14

O9HFH0 PRELIMINARY; PRT: 223 AA.
AC O9HFH0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Endo-1,4-xylanase precursor (EC 3.2.1.8).
GN XYN.
OS *Penicillium funiculosum*.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Penicillium*.
OX NCBI_TaxID=28572;
RN [1]
RP SEQUENCE FROM N.A.
RA Furniss C.S.M., Belshaw N.J., Alcocer M.J., Williamson G., Fish N.M.,
RT Kiron P.A.;
RT "Tight binding of a wheat xylanase inhibitor protein (XIP-1) to a
RT family 11 xylanase expressed homologically in *Penicillium*
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ278385; CAC15487.1; -.
DR HSSP: P36217; 1XTO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1
FT CHAIN 34 223
FT SIGNAL 16
FT CHAIN 16
SQ SEQUENCE 223 AA; 24045 MW; 428CD224C8F13C77 CRC64;

Query Match 62.0%; Score 647.9; DB 3; Length 223;
Best Local Similarity 61.4%; Pred. No. 1.2e-19;
Matches 113; Conservative 29; Mismatches 41; Indels 1; Gaps 1;
OY 7 TGYNNGYRYSYWNGHGVYTNTPGGQFYSVMNSNGNFVGKGNQPGTKNKVINFSSGY 66
DB 11 TGYNNGYRYSYWNGHGVYTNTPGGQFYSVMNSNGNFVGKGNQPGTKNKVINFSSGY 66

DB 41 TGTNNGYRYSEFTNGCGEVTYTNNGDNGEYVTWVDCGDFTSKGKNNPANA-OTVYISGF 99
OY 67 NPNNGNSYLSYVGMNRNPLEEYIVENFGYNSNSTGATKLGVTSGSYVDIYRTORVNP 126
DB 100 NPSGNAYLAVGWTDPLEVEYILEDYGDYNGNSMTYKGTVSDGSVYDIYRTORVNP 159
OY 127 SIIGTATFYQYWSVRNRHSSGSVNTANHFNMAAOGLTLGTMQIYAVEGYFSSGSAS 186
DB 160 STEGSTFNQYWSVTERKRGVYTNHFNMAKLGLEMGTYNIMYVSTEGYESSGST 219
OY 187 ITVS 190
DB 220 ITVS 223

RESULT 15

O13447 PRELIMINARY; PRT: 231 AA.
AC O13447;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Beta-1,4-xylanase.
GN XYL2.
OS *Cochliobolus sativus* (Bipolaris sorokiniana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; *Cochliobolus*.
OX NCBI_TaxID=45130;
RN [1]
RP SEQUENCE FROM N.A.
RA Emami K., Hack E.;
RT "Characterisation of a xylanase gene from *Cochliobolus sativus* and its
RT expression.";
RL Mycol. Res. 0:0-0(0).
DR EMBL: AJ004802; CAA06151.1; -.
DR HSSP: O43097; 1YNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 231 AA; 25577 MW; 333E6DD1F065A6BF CRC64;

Query Match 60.9%; Score 635.9; DB 3; Length 231;
Best Local Similarity 59.3%; Pred. No. 3.9e-19;
Matches 112; Conservative 26; Mismatches 50; Indels 1; Gaps 1;

OY 1 QTIDPGYNNNGYRYSYWNGHGVYTNTPGGQFYSVMNSNGNFVGKGNQPGTKNKVI 60
DB 41 QSTPSESEGYHNGYFYSMWTDGGSQYQYTMGGSRYSVYTRNTGNFVGKGNPPT-GRVI 99
OY 61 NFSGSYNPNNGNSYLSYVGMNRNPLEEYIVENFGYNSNSTGATKLGVTSGSYVDIYRT 120
DB 100 NYGAFNPGQNGYLAIVGWTNPLVEYIVIESYGTYPNSSQAQVKSFDTDGTYNAVS 159
OY 121 QRVNOPSISGTATFYQYWSVRNRHSSGSVNTANHFNMAAOGLTLGTMQIYAVEGYF 180
DB 160 TRYNOPSIDGRTITQYWSVQOKRGVGSVMQNHFNMAKLGLEMGTYNIMYVSTEGYESSGST 219
OY 181 SSGSASTIV 189
DB 220 SSGSSDIYV 228

RESULT 16

O8VUT4 PRELIMINARY; PRT: 346 AA.
AC O8VUT4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Beta-1,4-xylanase.

GN AYNA.
OS Pseudomonas sp. ND137.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=147640;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ND137;
RA Aoki Y., Kitamura E., Myouga H., Kamel Y.;
RT "Protoplast production of red alga Porphyra yezoensis by recombinant
enzymes from Pseudomonas sp.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB063255; BAB79287.1; -
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; UNKNOWN_1.
KW Xylan degradation; Hydrolase; Glycosidase.
SQ SEQUENCE 346 AA; 36749 MW; F247F48FAF73B9E CRC64;

Query Match 60.6%; Score 632.9; DB 2; Length 346;
Best Local Similarity 58.5%; Pred. No. 1.1e-18;
Matches 107; Conservative 34; Mismatches 41; Indels 1; Gaps 1;
QY 7 TGYNNGFYSYWMDHGVYTYTNGPGQFVSVMNSNGNFYGGKGMOPGTRKKVINFSGSY 66
DB 32 TGTGNGYYSFWMADPACTVSMITLGGSGNTSSQMSNTGMVGGKGMNNGGR-KRYSYSGTF 90
QY 67 NPGNSYLSYVGSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRTORVNOP 126
DB 91 NPGNGYLLTYGWTTPLEIYIVDMNGSYRPGESGTYGTVMDGCTYDIYRTORVNOP 150
QY 127 SIIGTATFYQYMGVRRHRSSGSVNTANHNMAAQCGLTGMDXQVAVAEGRFSSGS 186
DB 151 SIQGTATFYQYWSVRQKRGITTTGNHFDAMASHGLNHDYVMATEGYOSSGNSN 210
QY 187 ITV 189
DB 211 ITL 213

RESULT 17
P87037 PRELIMINARY; PRT: 221 AA.
ID P87037;
AC P87037;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE XYNGL.
GN XYNGL.
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eucotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KRN616;
RA Kimura T., Kitamoto N., Kito Y., Karita S., Sakka K., Ohmura K.;
RT Cloning and sequence of xylanase G1 gene from Aspergillus oryzae
KRN616.
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB003085; BAA19744.1; -
DR HSP: P36217; LYXO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
SQ SEQUENCE 221 AA; 23746 MW; C010E11E5F53C77E CRC64;

Query Match 60.4%; Score 631.3; DB 3; Length 221;
Best Local Similarity 56.2%; Pred. No. 5.6e-19;
Matches 113; Conservative 28; Mismatches 43; Indels 17; Gaps 2;

QY 5 PG-----TGYNNGFYSYWMDHGVYTYTNGPGQFVSVMNSNGNFVGC 48
DB 21 PGDSTLVELAKRAITSETGTNNGYYSFMTNGGDVEYIYNGNGQY-SVAMTNDNRYAG 80
QY 49 KGMOPGTRKKVINFSGSYNPNGNSYLSVGSRNPLIEYIVENFGTYNPSTGATKLGCV 108
DB 81 KGMNPGSA-KTVYTGSEMSNSYSVLYGMQNPFLVEYIVDKYDGDYDSTGATELGTV 139
QY 109 TSDGSVDIYRTORVNOPSLIGTATFYQYWSVRNRHSSGSVNTANHNMAAQCGLTGT 168
DB 140 ESDGTYKIKYTRRNAPSIEGTSFTNQYWSVRSGRVGGTITAQNHFDAMANYGLDGT 199
QY 169 MDYQIVAEVGEFSSGSATIV 189
DB 200 HNYMILATEGKSSGSATIV 220

RESULT 18
000350 PRELIMINARY; PRT: 231 AA.
ID 000350;
AC 000350;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Xyl2 precursor.
GN XYL2.
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB111;
RX MEDLINE=97055717; Pubmed=8900004;
RA Apel-Birkhold P.C., Walton J.D.;
RT Cloning, disruption, and expression of two endo-beta 1, 4-xylanase
genes, XYL2 and XYL3, from Cochliobolus carbonum.
RL Appl. Environ. Microbiol. 62:4129-4135(1996).
DR EMBL: U58915; AAC62815.1; -
DR HSP: O43097; IYNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal.
FT SIGNAL 1 41
FT CHAIN 41 231
FT CHAIN 41 231
SQ SEQUENCE 231 AA; 25576 MW; 237C3D49C4D0E871 CRC64;

Query Match 60.2%; Score 628.9; DB 3; Length 231;
Best Local Similarity 58.7%; Pred. No. 7.6e-19;
Matches 111; Conservative 26; Mismatches 51; Indels 1; Gaps 1;
QY 1 OTIQPGTYNNGFYSYWMDHGVYTYTNGPGQFVSVMNSNGNFYGGKGMOPGTRKKV 60
DB 41 OTSPSACGTYNNGFYSYWMDHGVYTYTNGPGQFVSVMNSNGNFYGGKGMNPGS-GRVI 99
QY 61 NFSGSYNPNNSYLSVGSRNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
DB 100 NYGAFNPQNGYLAIVGWTRNPLVEYIVESYCTVNPSSQAQKSGSFQDYGTYNAVS 159
QY 121 QRVNPSLIGTATFYQYWSVRNRHSSGSVNTANHNMAAQCGLTGTMDYQIVAEVGYF 180
DB 160 TRYNQPSIDGTRFYQYWSVTRORVGSVNMQNHFNAMSRYGGLNLDQHYQIVATEGYQ 219
QY 181 SSGSASITV 189
DB 220 SSGSSDITV 228

RESULT 19

P81536 PRELIMINARY: PRT: 194 AA.
 AC P81536: 01-JUN-2000 (TREMBlrel. 14, Created)
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
 DE xylanohydrolase) (PXY) (Fragment).
 OS Paecilomyces variotii.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.
 OX NCBI_TaxID=45996;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (1.59 ANGSTROMS), AND PARTIAL SEQUENCE.
 RC STRAIN-BARNIER:
 RA MEDLINE=20090955; PubMed=10623548;
 RA Kumar P.R., Eswaramoorthy S., Vithayathil P.J., Vismamitra M.A.;
 RT "The tertiary structure at 1.59 Å resolution and the proposed amino
 RT acid sequence of a family-11 xylanase from the thermophilic fungus
 RT Paecilomyces variotii baltner";
 RL J. Mol. Biol. 295:581-593(2000).
 CC -1- CATALYTIC ACTIVITY: ENDOLYXOLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR HSP: 043097: 1YNA.
 DR InterPro: IPR001137: GH_11.
 DR Pfam: PF00457: Glyco_hydro_11; 1.
 DR PRINTS: PR00911: GLHYDRASE11.
 DR PROSITE: PS00776: GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777: GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation: Hydrolase; Glycosidase; Acetylation.
 FT MOD_RES 1 1
 FT ACT_SITE 86 86 ACETYLATION.
 FT ACT_SITE 178 178 NUCLEOPHILE (BY SIMILARITY).
 FT DISULFID 110 154 PROTON DONOR (BY SIMILARITY).
 FT NON_TER 194 194
 SO SEQUENCE 194 AA; 20947 MW; 1D5C50AA4F6EDB90 CRC64;

Query Match 59.8%; Score 624.4; DB 3; Length 194;
 Best Local Similarity 59.7%; Pred. No. 8.4e-19;
 Matches 114; Conservative 26; Mismatches 45; Indels 6; Gaps 2;

QY 6 GT-----GYNNGYRYTWNDSHGCVYTYNGPGGQFSVNMNSGNGFVGKGMQPTKKNKYI 60
 DB 1 GTTPNSGGMHDGYYSWMSDGGDSTYTNNSGGTYEITWNGMNLVGKGNPGLNARAI 60
 QY 61 NFSGSYNPNNGNSYLSVGMGRNPLIEYIVENFGTYNPSTGATKLGVEYTSQGSYDIYRT 120
 DB 61 HFTGVYPNGTSTYLSVGMGRNPLIEYIVENFGSSNPSSTDLGVTSCGSGSTYTLGQS 120
 QY 121 ORVNPSPITGATFYQYVSRNRHSSGSVNTANHFNMAAQGLTL-GTMDYQIYAVEGY 179
 DB 121 TRVNPSPIDGTQTFNQVSWVRQDKRSSGTQGTGCHFDAMASAGLNVGDHDTQIVATIEGY 180
 QY 180 FSSGSASATVS 190
 DB 181 FSSGVARITVA 191

RESULT 20

O9HGE1 PRELIMINARY: PRT: 227 AA.
 AC O9HGE1: 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Beta-1,4-xylanase.
 GN XYN2.
 OS Humicola grisea var. thermolidea.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.

OX NCBI_TaxID=5528;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=60849;
 RA Faria F.P., Pocas-Fonseca M.J., Azevedo M.O.;
 RT "Cloning of a xylanase-encoding gene from the thermophilic fungus
 RT Humicola grisea and its expression in Escherichia coli.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF155594; AAC16891.1;
 DR HSP: 043097: 1YNA.
 DR InterPro: IPR001137: GH_11.
 DR Pfam: PF00457: Glyco_hydro_11; 1.
 DR PRINTS: PR00911: GLHYDRASE11.
 DR PROSITE: PS00776: GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777: GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase; Hydrolase; Xylan degradation.
 SO SEQUENCE 227 AA; 25615 MW; 991813AD8EB2939 CRC64;

Query Match 58.9%; Score 615.9; DB 3; Length 227;
 Best Local Similarity 59.3%; Pred. No. 2.5e-18;
 Matches 108; Conservative 25; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNNGYRYTWNDSHGCVYTYNGPGGQFSVNMNSGNGFVGKGMQPTKKNKYINFSGSYN 67
 DB 44 GHNNGYRYTWNDSHGCVYTYNGPGGQFSVNMNSGNGFVGKGMQPTKKNKYINFSGSYN 102
 QY 68 PNGNSYLSVGMGRNPLIEYIVENFGTYNPSTGATKLGVEYTSQGSYDIYRTORVNP 127
 DB 103 PNGNGYLAIVGWTNPLIEYIVENFGTYNPSTGATKLGVEYTSQGSYDIYRTORVNP 162
 QY 128 ITCATFYQYVSRNRHSSGSVNTANHFNMAAQGLTLGTMDOYIYAVEGYFSSGSASI 187
 DB 163 IDGTFQOYVSRNRHSSGSVNTANHFNMAAQGLTLGTMDOYIYAVEGYFSSGSASI 222
 QY 188 TV 189
 DB 223 YV 224

RESULT 21

O96UV7 PRELIMINARY: PRT: 283 AA.
 AC O96UV7: 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE XynIIA.
 GN XYNIIA.
 OS Lentinula edodes (Shiitake mushroom) (Lentinus edodes).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Lentinula.
 OX NCBI_TaxID=5353;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=STAMETS CS-2;
 RA Lee C.C., Wong D.W.S., Robertson G.H.;
 RT "Cloning and characterization of xylanase (xynIIA) from Lentinula
 RT edodes.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF411252: ALD04152.1;
 DR InterPro: IPR000254: CBD_Fungal.
 DR InterPro: IPR001137: GH_11.
 DR Pfam: PF00734: CBM_1; 1.
 DR Pfam: PF00457: Glyco_hydro_11; 1.
 DR ProDom: PD001821: CBD_Fungal; 1.
 DR PROSITE: PS00562: CBD_FUNGAL; 1.
 DR PROSITE: PS00777: GLYCOSYL_HYDROL_F11_2; UNKNOWN_1.
 SO SEQUENCE 283 AA; 29474 MW; A41B94A7F8677243 CRC64;

Query Match 58.7%; Score 613.9; DB 3; Length 283;
 Best Local Similarity 58.7%; Pred. No. 4.6e-18;
 Matches 111; Conservative 26; Mismatches 51; Indels 1; Gaps 1;

QY	1	OTIQPGCTNNNGYEFVSYNNDGCGVTTYNNPCGGQSVNMSNGNFVGGKGMQPGCTNNKYI	60
Db	32	RSIPNGEGTNNNGYEFVSYSDTTVTGTTTNGPGEGETLLMGSGGDVYVGGKGMGPMSV-	90
QY	61	NFSGSYNNGNSYLSYVCGMSRNPLEIYYIVENFGTYNPGTATKKGVEYSDGSVDIYRT	120
Db	91	EYSGYISPNNGNSYLSYVCGMHSPLVEYYIITDSFGDYNPSTGTGTLGCTGSDGVDIYRQ	150
QY	121	QRVNPSTIIGATFYQYVSVRRNRHSSGSVNTANHFNAWAQGLTGTMDYOIVAVEGYE	180
Db	151	TRTNAPSTIGCATFOQYWSIRQTHREVGCTVTGNGHXSCHESVGLPLGTENYIILATEGYS	210
QY	181	SSGSASTIV 189	
Db	211	SSGSTITIV 219	
RESULT 22			
Q9ROB8			
ID	Q9ROB8	PRELIMINARY:	PRT: 335 AA.
AC	Q9ROB8:		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Endo-1,4-beta-xylanase (EC 3.2.1.8).		
GN	XYN1A.		
OS	Cellulomonas pachnodae.		
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;		
CC	Actinomycetales; Micrococcales; Cellulomonadaceae; Cellulomonas.		
OX	NCBI_TaxID=101489;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99402156; PubMed=10473422;		
RA	Cazemier A.E., Verdoes J.C., van Ooyen A.J., Op den Camp H.J.;		
RT	"Molecular and biochemical characterization of two xylanase-encoding		
RL	genes from Cellulomonas pachnodae."		
DR	EMBL; AF120156; AAD54767.1; -		
DR	HSSP; P09850; 1XNB.		
DR	InterPro: IPR001919; Bac_cellose-bind.		
DR	InterPro: IPR001137; GH_11.		
DR	Pfam; PF00553; CBM_2; 1		
DR	Pfam; PF00457; Glyco_hydro_11; 1.		
DR	PRINTS; PR00911; GLHYDRLASE11.		
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.		
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.		
KM	Glycosidase: Hydrolase: xylan degradation.		
SO	SEQUENCE 335 AA; 34383 MW; 64FEDB80C25542D CRC64;		
Query Match			
	Best Local Similarity	58.5%; Score 611; DB 2; Length 335;	
	Matches 109; Conservative	32; Mismatches 42; Indels 10; Gaps 3	
QY	4	QP-----GTCYNNGYFYSYNDCHGCVTTYNGPQGGFVSVMNSGNFVGGKGMQPGTK	56
Db	40	QPAAAVDSNNSGSGGYEYFETWDAPGTVSMNLGSGGNGSTSMSTNGNVAACKGWSGSA	99
QY	57	NKVINFGSYNNGNSYLSYVCGMSRNPLEIYYIVENFGTYNPGTATKKGVEYSDGSVD	116
Db	100	RTISYSGTFNPSGNAIYAVGWSHDPLEIYIVDSWGYRPT--GTFNGYVNSDGGTYD	156
QY	117	IYRTQVNPSTIIGATFYQYVSVRRNRHSSGSVNTANHFNAWAQGLTGTMDYOIVAV	176
Db	157	IYKTRTNAPSTIGCATFYQYVSVQSKRVGSTITTANHFNAWSGMLGHRHDYIILAT	216
QY	177	EGYSSGSASTIV 189	
Db	217	EGYSSGSASNITI 229	
RESULT 23			
ID	008346	PRELIMINARY:	PRT: 335 AA.
008346			

[illegible]

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

DR Subtil: AF194025; AAF04601.1; -

DR HSSP: P09850.1XNB.

DR InterPro: IPR001919; Bac_cellose-bind.

DR InterPro: IPR001137; GH_11.

DR InterPro: IPR001230; Prenyl_site.

DR Pfam: PF00553; CBM_2; 1.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLHYDRLASE1.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

DR PROSITE: PS00794; PRENYLATON; UNKNOWN_1.

KW Signal.

FT SIGNAL.

FT CHAIN

SO SEQUENCE 335 AA; 35328 MM; D/DED/BACB52710 CRC64;

POTENTIAL.
XYLANASE B.

Query Match 58.4%; Score 610.7; DB 2; Length 335;
Best Local Similarity 59.6%; Pred. NO. 8.7e-18;
Matches 109; Conservative 28; Mismatches 43; Indels 3; Gaps 3.

OY TGNNNGYYYSWNDDHGGVTTNCGGGEFSVMNSGNFVGKGMQPTKKNVINFGSSY 66
Db |||::|||::||||::| | | | | | | | | | | | | | | | : ::||:::
48 TGTNHNGYTSFWTDAPRGVTYNTAGTGAAGNYSTGWMTGTFPVAGKGKATGR-RTYISGTF 106
OY NPNGNSLYSVYGWSRNPILIEEYIVENEGTYPNSTGATKLGEVSDGSVYDIPIRGQRNOP 126
Db |||::|||::||||::| | | | | | | | | | | | | | | | : ||:::
107 NPSGANAYALGVGSQNPPLVEYYYIDNMGYTP-RGTYK-GTVYSDGCTIYDIMTRYANP 164
OY SIGTAFFGYQWVSVRNRHRSGGSVYTAHFPMANOGLTLGTMDQIYAAGEYFESSGSAS 186
Db |||::|||::||||::| | | | | | | | | | | | | | | | : ||:::
165 SIETKTPTNOYWVSVRNQNKRTGCTITTGHHFDMAHMGMLCFTFNIMILLATEGYOSSGSSN 224
OY 187 ITV 189
Db |||
225 ITV 227

RESULT 25

ID O56265 PRELIMINARY; PRT: 338 AA.

AC O56265;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Endo 1,4-beta-D-xylanase precursor.

CN TPXA.

OS Thermomonospora fusca.

OC Bacteria; Firmicutes; Actinobacterlia; Actinobacteridae;

CC Actinomycetales; Streptosporangineae; Nocardiopsaceae; Thermoactidiales.

OX NCBI_TaxId=2021;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-YX:

RA MEDLINE=94213454; PubMed=8161173;

RT Irwin D., Jung E.D., Wilson D.B.;

RL "Characterization and sequence of a Thermomonospora fusca xylanase.";

RT Appl. Environ. Microbiol. 60:763-770(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-YX:

RA MEDLINE=89255048; PubMed=2656632;

RT Changas G.S., Hu Y.J., Wilson D.B.;

RL "Cloning of a Thermomonospora fusca xylanase gene and its expression in Escherichia coli and Streptomyces lividans.";

RT J. Bacteriol. 171:2963-2969(1989).

DR EMBL: U01242; AAA21480.1; -

DR HSSP: P09850.1XNB.

DR InterPro: IPR001137; GH_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLHYDRLASE1.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KM		Glycosidase; Hydrolase; Signal; Xylan degradation.
FT	SIGNAL	POTENTIAL.
FT	CHAIN	ENDO 1,4-BETA-D XYLANASE.
SO	SEQUENCE	338 AA; 36406 MW; 188AF3AA8430A3C7 CRC64;
 Query Match 58.2%; Score 608.7; DB 2; Length 338; Best Local Similarity 58.8%; Pred. No. 1,le-17; Matches 104; Conservative 37; Mismatches 39; Indels 3; Caps 2		
OY	7	TGTCNGCYFYSYNMDGHGGVTTTNGPGQFVSVMNSGNEFGKGMOPGTNRKNKYINFSGSY
Dd	49	TT
OY	67	NPNNGSYLSVCGSRNPLEIYEIVNFCTYNPSTGATLGEVTSDSGSVDIITRYOVNOP
Dd	108	NN
OY	127	SIIGTAIFYOYSVRNRHRSQSNTANHFMAAOGLTLTGMDYOIVAEGEYSSGSAS
Dd	166	III
OY	187	IIV 189
Dd	226	VTL 228
 RESULT 26 OGCI.R1 PRELMINARY; PRT: 231 AA. AC OGCI.R1: DT_01-JUN-2001 (TrEMBLrel. 17, Created) DT_01-JUN-2001 (TrEMBLrel. 17, Last sequence update) DT_01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE xylanase 4 protein. GN XYL4. OS Fusarium oxysporum f. sp. lycopersici. OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; OC Hypocreales; Mitosporic Hypocreales; Fusarium. OX NCBI_TaxID=59765; RN [1] RP SEQUENCE FROM N.A. RA Hera C., Gomez-Gomez E., Roncero M.; RT "Cloning and characterization of two family II xylanase genes in RT Fusarium oxysporum f. sp. lycopersici."; RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. DR EMBL; AFZ46831; AAK27975.1; - DR HSP; O43097; IYNA. DR Interpro; IPRO01137; GH_11. DR Pfam; PF00457; Glyco_hydro.11; 1. DR PRINTS; PRO0911; GLHYDRLASE11. DR PROSITE; PS00776; GLYCOSTYL_HYDROL_F11_1; 1. DR PROSITE; PS00777; GLYCOSTYL_HYDROL_F11_2; 1. SQ SEQUENCE 231 AA; 25638 MW; 94D26C66B7890792 CRC64;		
 Query Match 58.1%; Score 606.9; DB 3; Length 211; Best Local Similarity 57.7%; Pred. No. 6,le-18; Matches 105; Conservative 28; Mismatches 48; Indels 1; Caps 1		
OY	8	GYNNGCYFYSYNMDGHGGVTTTNGPGQFVSVMNSGNEFGKGMOPGTNRKNKYINFSGSYN
Dd	48	III
OY	68	PNCNSTSLASYGCSRNPYLEIYEIVNFCTYNPSTGATLGEVTSDSGSVDIITRYOVNOP
Dd	107	POONGILCYGVGTRPLVEIYEIVNFCTYNPSTGATLGEVTSDSGSVDIITRYOVNOP
OY	128	IICATAFYOYSVRNRHRSQSNTANHFMAAOGLTLTGMDYOIVAAGEVSSGSASI
Dd	167	III
OY	188	TV 189
Dd	227	YV 228

Query	Subject	Score	Expect	Ident	Length	Gaps
1	1	57.68	601.4	DB 2	228	
2	2	54.38	1e-17	41	Indels 16	Gaps 5
3	3	34	Mismatches			
4	4	34	Mismatches			
5	5	34	Mismatches			
6	6	34	Mismatches			
7	7	34	Mismatches			
8	8	34	Mismatches			
9	9	34	Mismatches			
10	10	34	Mismatches			
11	11	34	Mismatches			
12	12	34	Mismatches			
13	13	34	Mismatches			
14	14	34	Mismatches			
15	15	34	Mismatches			
16	16	34	Mismatches			
17	17	34	Mismatches			
18	18	34	Mismatches			
19	19	34	Mismatches			
20	20	34	Mismatches			
21	21	34	Mismatches			
22	22	34	Mismatches			
23	23	34	Mismatches			
24	24	34	Mismatches			
25	25	34	Mismatches			
26	26	34	Mismatches			
27	27	34	Mismatches			
28	28	34	Mismatches			
29	29	34	Mismatches			
30	30	34	Mismatches			
31	31	34	Mismatches			
32	32	34	Mismatches			
33	33	34	Mismatches			
34	34	34	Mismatches			
35	35	34	Mismatches			
36	36	34	Mismatches			
37	37	34	Mismatches			
38	38	34	Mismatches			
39	39	34	Mismatches			
40	40	34	Mismatches			
41	41	34	Mismatches			
42	42	34	Mismatches			
43	43	34	Mismatches			
44	44	34	Mismatches			
45	45	34	Mismatches			
46	46	34	Mismatches			
47	47	34	Mismatches			
48	48	34	Mismatches			
49	49	34	Mismatches			
50	50	34	Mismatches			
51	51	34	Mismatches			
52	52	34	Mismatches			
53	53	34	Mismatches			
54	54	34	Mismatches			
55	55	34	Mismatches			
56	56	34	Mismatches			
57	57	34	Mismatches			
58	58	34	Mismatches			
59	59	34	Mismatches			
60	60	34	Mismatches			
61	61	34	Mismatches			
62	62	34	Mismatches			
63	63	34	Mismatches			
64	64	34	Mismatches			
65	65	34	Mismatches			
66	66	34	Mismatches			
67	67	34	Mismatches			
68	68	34	Mismatches			
69	69	34	Mismatches			
70	70	34	Mismatches			
71	71	34	Mismatches			
72	72	34	Mismatches			
73	73	34	Mismatches			
74	74	34	Mismatches			
75	75	34	Mismatches			
76	76	34	Mismatches			
77	77	34	Mismatches			
78	78	34	Mismatches			
79	79	34	Mismatches			
80	80	34	Mismatches			
81	81	34	Mismatches			
82	82	34	Mismatches			
83	83	34	Mismatches			
84	84	34	Mismatches			
85	85	34	Mismatches			
86	86	34	Mismatches			
87	87	34	Mismatches			
88	88</					

```

RL Submitted (NOV-1999) to the EMBL/genbank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RM Submitted (Dec-1999) to the EMBL/genbank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RZ Redenbach M., Kieser H.M., Denaplatte D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RL the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RW Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Croun A., Fraser A., Goble A., Hidalgo J., Hornsbly T., Howarth S.,
Huang C.H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
Ra Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wetzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL colorator A3(2).";
RU Nature 417:141-147(2002).
DR EMBL: ALI33220; CAB61738.1; -.
DR HSSP: P09850; 1XNB.
DR InterPro: IPR001919; Bac_celose-bind.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00553; CBM_2; 1.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLYHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ
SEQUENCE   335 AA:  35533 MW: EC0d55E786CCFC0C2 CRC64:

Query Match      57.2% Score 597.4 DB 16 Length 335:
Best Local Similarity    55.1%, Pred. No. 3,le-17;
Matches 109; Conservative 31; Mismatches 42; Indels 16; Gaps 5

OY          5 PGT-----GYNNGFYFYNWNDGCHGVTTNPBGQGFVNMSNSGMFGVGKKMQ 52
               |||         |||||||:|||         ||||:|.:.|||:|||||
DbB       36 PGTAOADPTVTNTNEGHTGNNGNYTSWTDSOGCVSNMGSGGGYSTSWRRATGFNVAGKGA 95
OY        53 PGTAKKVTFNFSGSYPNCNSLYSVYGWSKNPLIEVIYEVEFTYSPSTGATFLGEVTDG 112
               :.:.|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DbB       96 NGCR-RITQYQSSEFNPSGCNAVLTALCGWISNPLEYIVIDNMGTTPR-IDCYR-CITYSDG 152
OY       113 SVYDIYTRQRNQESICTATIFYQYSVARNRHRSSGSVNTANHEPNAAQQGLTLGMT-D-Y 171
               |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DbB     153 GTYDYIKTKTIRVANKPEVECTRTFDQYSVRQAOKRTGTLTGNNHPAMARACMLPGNFSY 212
OY       172 QIVAVEGESGASASTVV 189
                |::|::|:|:|:|:|:|
DbB     213 MIIMATEGYOSSGSSSIINV 230

RESULT  29
O74716 PRELIMITARY: PRT: 216 AA.
ID O74716 AC
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
GN xylI.
OS Claviceps purpurea (Ergot fungus)
```

CC Eukaryote: Fungi: Ascomycota: Pezizomycotina: Sordariomycetes;
OC Hypocreales: Clavicipitaceae: Claviceps.
OX NCBI_TaxID=5111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=75;
RA Giesbert S., Lepping H.B., Tenberge K.B., Tudzynski P.;
RT "The xylanolytic system of *Claviceps purpurea*: cytological evidence
for secretion of xylanases in infected rye tissue and molecular
characterization of two xylanase genes.";
RL Phytopathology 88:1020-1030(1998).
DR EMBL: Y16969; CAA76570.1; -
DR HSSP: P36217; 1XVO.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Glycosidase: Hydrolase: Signal; Xylan degradation.
FT SIGNAL
FT SEQUENCE 216 AA; 23339 MW; 012E874E939E7581 CRC64;

Query Match 57.1%; Score 596.8; DB 3; Length 216;
Best Local Similarity 58.2%; Pred. No. 1.4e-17;
Matches 106; Conservative 29; Mismatches 45; Indels 2; Gaps 2;

QY 9 YNNGEYSYWNDHGVTYTNPGGQFVSVMNSGNEFVGKGNQPGTKNKVINFGSGSYN 68
ID 09RMH9 PRELIMINARY; PRT; 329 AA.
AC 09RMH9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Xylanase.
GN SVXA.
OS Streptomyces viridosporus.
OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
OX NCBI_TaxID=67581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=77A;
RA Kanhyur D.N., Magnuson T.S., Crawford D.L.;
RT "Cloning, sequencing and characterization of the xylanase-encoding
rt gene svxa, from *Streptomyces viridosporus* T7A, and its expression in
rt *Escherichia coli*.";
RL Nippon Hosenkin Gakkaishi 0:0-0(2000).
DR EMBL: AF198618; AAF09501.1; -
DR HSSP: P09850; 1XNB.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN.1
SQ SEQUENCE 329 AA; 35132 MW; 7E9C7A625664E637 CRC64;

Query Match 56.9%; Score 594.5; DB 2; Length 329;
Best Local Similarity 54.5%; Pred. No. 3.9e-17;
Matches 108; Conservative 32; Mismatches 43; Indels 15; Gaps 4;
QY 5 PGT-----GYNNGEYSYWNDHGVTYTNPGGQFVSVMNSGNEFVGKGNQ 52
ID 09EM89 PRELIMINARY; PRT; 191 AA.
AC 09EM89;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-xylanase (EC 3.2.1.8) (Fragment).
GN GXYN.
OS Streptomyces olivaceoviridis (Streptomyces corchorus11).
OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
OX NCBI_TaxID=1921;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-86;
RA Bin Y.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=E-86;
RA Zhang H., Yao B., Wang Y.;
RT "Cloning and expression of the 23kd beta-xylanase gene from
RT Streptomyces olivaceoviridis E-86.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A2929217; CAC19491.1; -
DR HSSP: P09850; 1XNB.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase: Hydrolase: Xylan degradation.
FT NON_TER
FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

Query Match 54.4%; Score 568.6; DB 2; Length 191;
Best Local Similarity 55.1%; Pred. No. 1.6e-16;
Matches 102; Conservative 32; Mismatches 47; Indels 4; Gaps 4;

QY 7 TGYNNGEYSYWNDHGVTYTNPGGQFVSVMNSGNEFVGKGNQPGTKNKVINFGSGY 66
ID 09EM89 PRELIMINARY; PRT; 191 AA.
AC 09EM89;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Beta-xylanase (EC 3.2.1.8) (Fragment).
GN GXYN.
OS Streptomyces olivaceoviridis (Streptomyces corchorus11).
OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
OX NCBI_TaxID=1921;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-86;
RA Zhang H., Yao B., Wang Y.;
RT "Cloning and expression of the 23kd beta-xylanase gene from
RT Streptomyces olivaceoviridis E-86.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A2929217; CAC19491.1; -
DR HSSP: P09850; 1XNB.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase: Hydrolase: Xylan degradation.
FT NON_TER
FT SEQUENCE 191 AA; 20781 MW; 7E1C45AADE1B6B9C CRC64;

[illegible]

```

OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=A3(2);
RC Oliver K., Harris D.;
RA Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
RL [2] SEQUENCE FROM N.A.
RR STRAIN=A3(2);
RC Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RA Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
RN [3] SEQUENCE FROM N.A.
RP STRAIN=A3(2);
RC MEDLINE=97000351; PubMed=8843436;
RX Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
RA Kinash H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RL Mol. Microbiol. 21:77-96(1996).
RN [4] SEQUENCE FROM N.A.
RP STRAIN=A3(2) / M45;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Lake L., Mulvey L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL Nature 417:141-147(2002).
DR EMBL; AL109949; CAB52919.1; -.
DR HSSP; P08950; 1XNB.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosylase; Hydrolase; Xylan degradation.
SQ SEQUENCE 241 AA; 25845 MW; 37B6E99DE517B78F CRC64;

Query Match          51.3%; Score 536.3; DB 16; Length 241;
Best Local Similarity 50.0%; Pred. NO. 5.4e-15;
Matches 100; Conservative 34; Mismatches 49; Indels 17; Gaps 6

OY      5  PGTGY-----NNGYEFSYVNDHGVTNTNGPGGQSVNMNSGNFVGKGMP   53
Db       ||| :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
         44  PGTAHAATTITNTQTGDGMYYSFWTDDGGGSVMTLNNGGSGYSTQMTNCGNFVAGKWSI   103
OY      54  GTKKVNIFFSSSYNNGNSLYLVGMSRPLLEYIVENFGTYNNSTGATKLGEVTSIDS   113
Db       | : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
         104  GGR-RTVANYNIEFNPSGNGCYGLGWTSPNLEVIYVDWMSGYRP-TGYRK-GTVSSDDG   160
OY     114  VDIYPTGVNQPISLTGATEFYQVYSVRNRHSSCS--VTANHFNAQAQGLTIGTM-D    170
Db       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
         161  TYDIYQTRVNAVSEGTGKTFOQVYVSVAQSKVTSSTGTTITCNHFDAMARACMNMQFRY   220
OY     171  YQYVAVEGFSSGSASITVS 190
Db       | : | : | | | | : | | |
         221  YMIMATEGYOSSGSNSTITS 240

RESULT 34
ID 052375 PRELIMINARY: PRT: 361 AA.
AC 052375;
JT 01-JUN-1998 (TREMBLrel .06, Created)
BT 01-JUN-1998 (TREMBLrel .06, Last sequence update)
```


Oy	180	FSSGSASIT	188
		..	
Db	211	OSSGSANIT	219
 RESULT 37			
ID	Q56013	PRELIMINARY:	PRT; 240 AA.
AC	Q56013.		
Dt	01-NOV-1996	(TREMBLrel. 01,	Created)
Dt	01-NOV-1996	(TREMBLrel. 01,	Last sequence update)
Dt	01-MAR-2002	(TREMBLrel. 20,	Last annotation update)
DE	Xylanase precursor.		
OS	Streptomyces sp. EC3.		
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;		
CC	Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.		
OX	NCBI_TaxID=993388;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-EC3:		
RA	MEDLINE=96293859; PubMed=8722569;		
RA	Mazy-Servais C., Moreau A., Gerard C., Dusart J.;		
RT	"Cloning and sequencing of a xylanase-encoding gene from Streptomyces		
RT	sp. EC3.";		
RL	DNA Seq. 6:147-158(1996).		
DR	EMBL: X81045; CA56935.1; -.		
DR	HSSP: P09850; 1XNB.		
DR	InterPro: IPR001137; GH_11.		
DR	Pfam: PF00457; Glyco_hydro_11; 1.		
DR	PRINTS: PR00911; GLHYDRIASE1.		
DR	PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.		
KW	PROSITE, PS00777; GLYCOSYL_HYDROL_F11_2; 1.		
FT	Signal.	1	49
FT	SIGNAL.		POTENTIAL.
FT	CHAIN	50	240
SO	SEQUENCE	240 AA;	25949 MM; SDBB864A4497FC3 CRC64;
 Query Match 50.5%; Score 527.4; DB 2; Length 240: Best Local Similarity 53.8%; Pred. No. 1.2e-14; Matches 100; Conservative 31; Mismatches 49; Indels 6; Gaps 6;			
Oy	7	TGYNNGEYTSWNNGHGVTYTNCGGCFSVMSNSGNFVGKGMQPTKKNVINFSGSY	66
	: : : : : : : : : : : : : : : :		
Db	58	TGY-DGMYRSWTDDGGSVSMTLNKGSIYTQMTNCGAFVAGKGNNGR-RIVATSGVF	115
Oy	67	NPNGNSTLSVYGWSRNPLIEYYIVEFGTYNPSTGATKLGEVTSDSVYDIYRTQRVNQP	126
	: : : : : : : : : : : : : : : :		
Db	116	NPSGNGCYCLTGCMSPNLVEYYIYVDNMGSYP-TGEYR-GTVYSDBGTYDIYIKTRYNAP	173
Oy	127	SIICTAFPEYOYWSVRNRH-RSSGSNTNHNHNNAAOGLTGTMD-YQIVAVEGFSSGS	184
	: : : : : : : : : : : : : : : :		
Db	174	SVECTRFDQYVSQRSKVIGSGITTTGNHRFDAMARAQMILGFOFYVMIMATEGYOSSGS	233
Oy	185	ASITVS 190	
	: :		
Db	234	SNITVS 239	
 RESULT 38			
ID	Q9KEF3	PRELIMINARY:	PRT; 210 AA.
AC	Q9KEF3.		
Dt	01-OCT-2000	(TREMBLrel. 15	Created)
Dt	01-OCT-2000	(TREMBLrel. 15,	Last sequence update)
Dt	01-JUN-2002	(TREMBLrel. 21,	Last annotation update)
DE	Endo-1,4-beta-xylanhydrolase.		
GN	BH0899.		
OS	Bacillus halodurans.		
CC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;		
CC	Bacillaceae; Bacillus.		
DX	NCBI_TaxID=86665;		
RN	[1]		

Q8RMN9 PRELIMINARY: PRT: 213 AA.
 AC Q8RMN9;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endo-1,4-xylinase.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sun J., Gu S., Li W., Xu Z., Zhao H., Xiao J., Fu L.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 KW EMBL: AF490979; AAC08359.1;
 KM Xylan degradation; Hydrolase; Glycosidase.
 SO SEQUENCE 213 AA; 23277 MW; 34DFAD49C2C0034 CRC64;

Query Match 46.6%; Score 487.2; DB 2; Length 213;
 Best Local Similarity 52.7%; Pred. No. 4,5e-13;
 Matches 96: Conservative 29; Mismatches 49; Indels 8; Gaps 6;

QY 14 FSTYNDCHGVTYTTNGGOFVSVMNSGNFVGKGMQPTKKNVINF-SGSIYPNGNS 72
 Db 33 YWQMTDGGGIVNAVNSGNGVSNMNTGNFVVGKGTSGPRTINYNAGVMAPNGNG 92
 QY 73 YLSVYGNRNPLIEYIYENFGTYNPSGATKLGFEVTSYDIYRTQRYNQPSITIG-T 131
 Db 93 YLTIGKTRSPLEIYIYVDSKGTYP-TGYTK-GTVKSDGGTYDITTRINAPSIDDR 150
 QY 132 ATFYQVMSVRNRHSSGS---VNTANHFNAMAQOGLTGT-MDYOIVAVEGFSSGSASI 187
 Db 151 TTFMQYCVQTKRPTGSMATITFSNHVDAMKSHGMNLSMAYVMAETEGQSSGSNV 210
 QY 188 TV 189
 Db 211 TV 212

RESULT 49
 087118 PRELIMINARY: PRT: 457 AA.
 AC 087118;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Xylanase.
 GN XYNB.
 OS Clostridium thermocellum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-F1;
 RX MEDLINE-99239090; PubMed-10222584;
 RA Hayashi H., Takehana M., Hattori T., Kimura T., Karita S., Sakka K.,
 RA Ohmura K.;
 "Nucleotide sequences of two contigations and highly homologous xylanase
 genes xyna and xynb and characterization of xyna from Clostridium
 thermocellum.";
 RT Appl. Microbiol. Biotechnol. 51:348-357(1999).
 RL EMBL: AB010958; BAA3542.1;
 DR HSSP: P36217; IXYO.
 DR InterPro: IPR005084; CBM_6.
 DR InterPro: IPR002105; Dockerin_1.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF03422; CBM_6; 1.
 DR Pfam: PF00404; Dockerin_1; 2.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRASE11.

DR PROSITE: PS00448; CLOS_CELLULOSE_RPT; 2.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; UNKNOWN_1.
 SO SEQUENCE 457 AA; 49884 MW; 86A8C048BD1224C5 CRC64;

Query Match 45.8%; Score 478.7; DB 2; Length 457;
 Best Local Similarity 49.7%; Pred. No. 4,3e-12;
 Matches 96: Conservative 26; Mismatches 58; Indels 13; Gaps 6;

QY 4 QPGTYNNGYFYSYND-GHGGVYTTNPGGOFVSVMNSGNFVGKGMQ-PGTRKNK--- 58
 Db 36 QGTG--GGYNEFYWKDTGNG--TWVLKDGGAFCSECSNINNLIFRKGFYDETRTHQOL 91
 QY 59 ---VINFGSNPNNGNSYLSYVGNRNPLIEYIYENGTNPSGATKLGFEVSDGSY 115
 Db 92 GTIYVTSCTNPNGNSYLSYVGNRNPLIEYIYENGTNPSGATKLGFEVSDGSY 150
 QY 116 DIYRTQRYNQPSITIGATFYQVMSVRNRHSSGSVNTANHFNAMAQOGLTGTMDYOIVA 175
 Db 151 EYETTRVNPQSIKGTATFOQYWSVTSKRTSGTISVTEHFKAMERLGMKMGKMEVALV 210
 QY 176 VEGYSSGSASTT 188
 Db 211 VEGYSSGSADVT 223

RESULT 50
 052779 PRELIMINARY: PRT: 457 AA.
 AC 052779;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Xylanase V.
 GN XYNV.
 OS Clostridium thermocellum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fernandes A.C., Fontes C.M.G.A., Clarke J.H., Hazlewood G.P.,
 RA Gilbert H.J., Fernandes T.H., Ferreira L.M.A.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF047761; AAC04578.1;
 DR HSSP: P36217; IXYO.
 DR InterPro: IPR005084; CBM_6.
 DR InterPro: IPR002105; Dockerin_1.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF03422; CBM_6; 1.
 DR Pfam: PF00404; Dockerin_1; 2.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRASE11.
 DR PROSITE: PS00448; CLOS_CELLULOSE_RPT; 2.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; UNKNOWN_1.
 SO SEQUENCE 457 AA; 49964 MW; 637DF52A0DACF889 CRC64;

Query Match 45.7%; Score 477.9; DB 2; Length 457;
 Best Local Similarity 49.5%; Pred. No. 4,6e-12;
 Matches 94: Conservative 27; Mismatches 56; Indels 11; Gaps 5;

QY 7 TGYNNGYFYSYND-GHGGVYTTNPGGOFVSVMNSGNFVGKGMQ-PGTRKNK----- 58
 Db 37 TGTGYNFYWKDTGNG--TWVLKDGGAFCSECSNINNLIFRKGFYDETRTHQOLGYI 94
 QY 59 VINFGSNPNNGNSYLSYVGNRNPLIEYIYENGTNPSGATKLGFEVSDGSYVDTY 118
 Db 95 TTYVTSCTNPNGNSYLSYVGNRNPLIEYIYENGTNPSGATKLGFEVSDGSYVDTY 153

Tue Jul 1 13:01:52 2003

us-09-990-874-16.rspt

Page 20

Oy	119	RTORNOSSITIGTAFFYYWYSVRNHRHSGGSANTANHFENAAOGLTLCIMDYQYAVAGC	178
		: : :	
Db	154	ETTRNGNSIKGTATFQQYMWSVRSTKRSCTISVIEHFKAMERLGMKKMKMEVALVDS	213
Oy	179	YFSSGASAIT	188
		: :	
Db	214	YQSSCKADVT	223

```
Search completed: July 1, 2003, 11:50:53
Job time : 82 secs
```